

Query Match 3.2%; Score 87.5; DB 7; Length 1197;
 Best Local Similarity 22.0%; Pred. No. 73;
 RESULT 1413
 ID ADO19438 standard; protein; 1197 AA.
 DE Human PRO polypeptide #184.
 PN WO2004043361-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match 3.2%; Score 87.5; DB 8; Length 1197;
 Best Local Similarity 22.0%; Pred. No. 73;
 RESULT 1414
 ID AAM79159 standard; protein; 1452 AA.
 DE Human protein SEQ ID NO 1821.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.2%; Score 87.5; DB 4; Length 1452;
 Best Local Similarity 25.9%; Pred. No. 99;
 RESULT 1415
 ID ABR58629 standard; protein; 1452 AA.
 DE Human cancer related protein SEQ ID NO:286.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 3.2%; Score 87.5; DB 6; Length 1452;
 Best Local Similarity 25.9%; Pred. No. 99;
 RESULT 1416
 ID ADJ68277 standard; protein; 1452 AA.
 DE Human heat mitochondrial protein as a therapeutic target SeqID83.
 PN WO2003087768-A2.
 PD 23-OCT-2003.
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 Query Match 3.2%; Score 87.5; DB 7; Length 1452;
 Best Local Similarity 25.9%; Pred. No. 99;
 RESULT 1417
 ID ADI80761 standard; protein; 1452 AA.
 DE Human protein tyrosine phosphatase receptor type mu protein sequence.
 PN US2004014699-A1.
 PD 22-JAN-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 3.2%; Score 87.5; DB 8; Length 1452;
 Best Local Similarity 25.9%; Pred. No. 99;
 RESULT 1418
 ID AAM80143 standard; protein; 1455 AA.
 DE Human protein SEQ ID NO 3789.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.2%; Score 87.5; DB 4; Length 1455;
 Best Local Similarity 25.9%; Pred. No. 99;
 RESULT 1419
 ID ABR53450 standard; protein; 1597 AA.
 DE Protein sequence #SEQ ID 1765.
 PN EP1258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.

Query Match 3.2%; Score 87.5; DB 6; Length 1597;
 Best Local Similarity 22.1%; Pred. No. 1.1e+02;

RESULT 1420
 ID ADK64624 standard; protein; 1597 AA.
 DE Disease treating protein complex-derived protein #1063.
 PN EP1338608-A2.
 PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Query Match 3.2%; Score 87.5; DB 7; Length 1597;
 Best Local Similarity 22.1%; Pred. No. 1.1e+02;

RESULT 1421
 ID ADO44172 standard; protein; 6885 AA.
 DE Structural and cytoskeleton-associated polypeptide #8.
 Query Match 3.2%; Score 87.5; DB 8; Length 6885;
 Best Local Similarity 18.6%; Pred. No. 1.1e+03;

RESULT 1422
 ID AAM21511 standard; protein; 69 AA.
 DE Peptide #7945 encoded by probe for measuring cervical gene expression.
 PN WO200157278-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 3.1%; Score 87; DB 4; Length 69;
 Best Local Similarity 29.2%; Pred. No. 0.96;

RESULT 1423
 ID ABB43855 standard; peptide; 69 AA.
 DE Peptide #11361 encoded by human foetal liver single exon probe.
 PN WO200157277-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 3.1%; Score 87; DB 4; Length 69;
 Best Local Similarity 29.2%; Pred. No. 0.96;

RESULT 1424
 ID AAM37766 standard; protein; 69 AA.
 DE Peptide #11803 encoded by probe for measuring placental gene expression.
 PN WO200157272-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 3.1%; Score 87; DB 4; Length 69;
 Best Local Similarity 29.2%; Pred. No. 0.96;

RESULT 1425
 ID ABB26783 standard; protein; 69 AA.
 DE Protein #8782 encoded by probe for measuring heart cell gene expression.
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 3.1%; Score 87; DB 4; Length 69;
 Best Local Similarity 29.2%; Pred. No. 0.96;

RESULT 1426
 ID AAM77581 standard; protein; 69 AA.
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 37887.
 PN WO200157276-A2.
 PD 09-AUG-2001.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 Query Match 3.1%; Score 87; DB 4; Length 69;
 Best Local Similarity 29.2%; Pred. No. 0.96;

RESULT 1427
 ID AAM64832 standard; protein; 69 AA.

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 36937.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.1%; Score 87; DB 4; Length 69;
Best Local Similarity 29.2%; Pred. No. 0.96;
RESULT 1428
ID ABG59228 standard; peptide; 69 AA.
DE Human liver peptide, SEQ ID No 37876.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.1%; Score 87; DB 4; Length 69;
Best Local Similarity 29.2%; Pred. No. 0.96;
RESULT 1429
ID ABG46614 standard; peptide; 69 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36279.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 3.1%; Score 87; DB 5; Length 69;
Best Local Similarity 29.2%; Pred. No. 0.96;
RESULT 1430
ID ABP25680 standard; protein; 250 AA.
DE Streptococcus polypeptide SEQ ID NO 536.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 3.1%; Score 87; DB 5; Length 250;
Best Local Similarity 24.7%; Pred. No. 7.1;
RESULT 1431
ID AAW72573 standard; protein; 356 AA.
DE Human glycosaminoglycan sulphate group transferase.
PN JP10257896-A.
PD 29-SEP-1998.
PA (SEK) SEIKAGAKU KOGYO CO LTD.
Query Match 3.1%; Score 87; DB 2; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;
RESULT 1432
ID AAB94514 standard; protein; 356 AA.
DE Human protein sequence SEQ ID NO:15229.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 3.1%; Score 87; DB 4; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;
RESULT 1433
ID ABB82859 standard; protein; 356 AA.
DE HS2ST related polypeptide (GenBank Identifier No. GI#6683564).
PN WO200299138-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 3.1%; Score 87; DB 6; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;
RESULT 1434
ID ABB82860 standard; protein; 356 AA.

DE HS2ST related polypeptide (GenBank Identifier No. GI#6912420).
PN WO200299138-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 3.1%; Score 87; DB 6; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;

RESULT 1435

ID ABU62934 standard; protein; 356 AA.
DE Human heparan sulphate 2-O-sulphotransferase HS2ST #1.
PN US2003013144-A1.
PD 16-JAN-2003.
PA (FRIE/) FRIEDMAN L.
PA (PLOW/) PLOWMAN G D.
PA (BELV/) BELVIN M.
PA (FRAN/) FRANCIS-LANG H.
PA (LIDD/) LI D.
PA (FUNK/) FUNKE R P.

Query Match 3.1%; Score 87; DB 6; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;

RESULT 1436

ID ABU62935 standard; protein; 356 AA.
DE Human heparan sulphate 2-O-sulphotransferase HS2ST #2.
PN US2003013144-A1.
PD 16-JAN-2003.
PA (FRIE/) FRIEDMAN L.
PA (PLOW/) PLOWMAN G D.
PA (BELV/) BELVIN M.
PA (FRAN/) FRANCIS-LANG H.
PA (LIDD/) LI D.
PA (FUNK/) FUNKE R P.

Query Match 3.1%; Score 87; DB 6; Length 356;
Best Local Similarity 20.2%; Pred. No. 12;

RESULT 1437

ID AAY36994 standard; protein; 431 AA.
DE Chlamydia trachomatis lipoprotein sequence.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.

Query Match 3.1%; Score 87; DB 2; Length 431;
Best Local Similarity 20.8%; Pred. No. 17;

RESULT 1438

ID AAW98588 standard; protein; 488 AA.
DE H. pylori GHPO 87 protein.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.1%; Score 87; DB 2; Length 488;
Best Local Similarity 19.5%; Pred. No. 20;

RESULT 1439

ID AAR10378 standard; protein; 514 AA.
DE Mutant alpha-amylase gene product.
PN EP409299-A.
PD 23-JAN-1991.
PA (KONN) GIST-BROCADES NV.

Query Match 3.1%; Score 87; DB 2; Length 514;
Best Local Similarity 21.8%; Pred. No. 22;

RESULT 1440

ID AAB12430 standard; protein; 514 AA.
DE Bacillus amyloliquefaciens clone number 22 protein SEQ ID NO:3.
PN JP2000135093-A.
PD 16-MAY-2000.
PA (DAIW) DAIWA KASEI KK.

Query Match 3.1%; Score 87; DB 3; Length 514;
Best Local Similarity 22.3%; Pred. No. 22;

RESULT 1441

ID AAB68551 standard; protein; 551 AA.
DE Human GTP-binding associated protein #51.
PN WO200105970-A2.
PD 25-JAN-2001.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 3.1%; Score 87; DB 4; Length 551;
Best Local Similarity 19.7%; Pred. No. 25;

RESULT 1442

ID AAB94384 standard; protein; 551 AA.
DE Human protein sequence SEQ ID NO:14939.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.

Query Match 3.1%; Score 87; DB 4; Length 551;
Best Local Similarity 19.7%; Pred. No. 25;

RESULT 1443

ID ADP54518 standard; protein; 551 AA.
DE Human PRO protein sequence SEQ ID NO:494.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.

Query Match 3.1%; Score 87; DB 8; Length 551;
Best Local Similarity 19.7%; Pred. No. 25;

RESULT 1444

ID AAB14796 standard; protein; 565 AA.
DE TGF-beta type II receptor.
PN US6093547-A.
PD 25-JUL-2000.
PA (CREA-) CREATIVE BIOMOLECULES INC.

Query Match 3.1%; Score 87; DB 3; Length 565;
Best Local Similarity 23.2%; Pred. No. 25;

RESULT 1445

ID ADN61899 standard; protein; 577 AA.
DE Human novel protein NOV56a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENA/) PENA C E A.
PA (LILL/) LI L.
PA (ZERH/) ZERHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWW/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEKU/) KEKUDA R.

PA (PATT/) PATTURAJAN M.
PA (GANG/) GANGOLLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEV V T.
PA (FERN/) FERNANDES E R.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATT/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.

Query Match 3.1%; Score 87; DB 8; Length 577;
Best Local Similarity 19.6%; Pred. No. 26;

RESULT 1446

ID AAW83995 standard; protein; 893 AA.
DE The DNA polymerase mutant D137A, D323A, R722N, F730Y.
PN WO9835060-A1.
PD 13-AUG-1998.
PA (LIFE-) LIFE TECHNOLOGIES INC.

Query Match 3.1%; Score 87; DB 2; Length 893;
Best Local Similarity 19.7%; Pred. No. 52;

RESULT 1447

ID ADC37548 standard; protein; 930 AA.
DE Human nucleic acid associated protein, NAAP-15.
PN WO2003046151-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.

Query Match 3.1%; Score 87; DB 7; Length 930;
Best Local Similarity 19.9%; Pred. No. 55;

RESULT 1448

ID ADC95237 standard; protein; 944 AA.
DE E. faecium protein sequence SEQ ID 4864.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 3.1%; Score 87; DB 7; Length 944;
Best Local Similarity 19.1%; Pred. No. 57;

RESULT 1449

ID ABP27459 standard; protein; 1034 AA.
DE Streptococcus polypeptide SEQ ID NO 4094.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 3.1%; Score 87; DB 5; Length 1034;
Best Local Similarity 18.7%; Pred. No. 65;

RESULT 1450

ID AAU35929 standard; protein; 1167 AA.
DE Helicobacter pylori cellular proliferation protein #242.

PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 3.1%; Score 87; DB 4; Length 1167;
 Best Local Similarity 18.8%; Pred. No. 79;
 RESULT 1451
 ID ABR53378 standard; protein; 1411 AA.
 DE Protein sequence #SEQ ID 1621.
 PN EP1258494-A1.
 PD 20-NOV-2002.
 PA (CELL-) CELLZOME AG.
 Query Match 3.1%; Score 87; DB 6; Length 1411;
 Best Local Similarity 24.5%; Pred. No. 1.1e+02;
 RESULT 1452
 ID ADK63342 standard; protein; 1411 AA.
 DE Disease treating protein complex-derived protein #982.
 PN EP1338608-A2.
 PD 27-AUG-2003.
 PA (CELL-) CELLZOME AG.
 Query Match 3.1%; Score 87; DB 7; Length 1411;
 Best Local Similarity 24.5%; Pred. No. 1.1e+02;
 RESULT 1453
 ID ABR47539 standard; protein; 1855 AA.
 DE Breast cancer associated protein sequence SEQ ID NO:315.
 PN WO2003004989-A2.
 PD 16-JAN-2003.
 PA (MILL-) MILLENIUM PHARM INC.
 Query Match 3.1%; Score 87; DB 6; Length 1855;
 Best Local Similarity 22.1%; Pred. No. 1.6e+02;
 RESULT 1454
 ID ADN04056 standard; protein; 1855 AA.
 DE Antipsoriatic protein sequence #223.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 87; DB 8; Length 1855;
 Best Local Similarity 22.1%; Pred. No. 1.6e+02;
 RESULT 1455
 ID ABB67961 standard; protein; 293 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 30675.
 PN WO200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 3.1%; Score 86.5; DB 4; Length 293;
 Best Local Similarity 21.1%; Pred. No. 10;
 RESULT 1456
 ID AAU38041 standard; protein; 352 AA.
 DE Streptococcus pneumoniae cellular proliferation protein #470.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 352;
 Best Local Similarity 29.2%; Pred. No. 14;
 RESULT 1457
 ID ABU23929 standard; protein; 359 AA.
 DE Protein encoded by Prokaryotic essential gene #9456.
 PN WO200277183-A2.

PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 359;
 Best Local Similarity 18.7%; Pred. No. 14;
 RESULT 1458
 ID AAG42135 standard; protein; 369 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 52510.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 3.1%; Score 86.5; DB 3; Length 369;
 Best Local Similarity 21.8%; Pred. No. 15;
 RESULT 1459
 ID AAB61228 standard; protein; 498 AA.
 DE Human TANGO 325 extracellular domain.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 498;
 Best Local Similarity 21.3%; Pred. No. 24;
 RESULT 1460
 ID ADB90766 standard; protein; 498 AA.
 DE Human TANGO 325 extracellular domain.
 PN US2003082586-A1.
 PD 01-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 7; Length 498;
 Best Local Similarity 21.3%; Pred. No. 24;
 RESULT 1461
 ID ADF71501 standard; protein; 498 AA.
 DE Human TANGO 325 extracellular domain.
 PN US2003175733-A1.
 PD 18-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 7; Length 498;
 Best Local Similarity 21.3%; Pred. No. 24;
 RESULT 1462
 ID ADM42026 standard; protein; 498 AA.
 DE Human TANGO 325 extracellular domain.
 PN US2003170621-A1.
 PD 11-SEP-2003.
 PA (MCCA/) MCCARTHY S A.
 PA (FRAS/) FRASER C C.
 PA (SHAR/) SHARP J D.
 PA (BARN/) BARNES T M.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (WRIG/) WRIGHTON N.
 PA (GOOD/) GOODEARL A D J.
 PA (HOLT/) HOLTZMAN D A.
 PA (KHOD/) KHODADOUST M.
 Query Match 3.1%; Score 86.5; DB 7; Length 498;
 Best Local Similarity 21.3%; Pred. No. 24;
 RESULT 1463
 ID ADI36908 standard; protein; 498 AA.
 DE Human LRR protein #3.
 PN US2003220263-A1.
 PD 27-NOV-2003.

PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 Query Match 3.1%; Score 86.5; DB 8; Length 498;
 Best Local Similarity 21.3%; Pred. No. 24;
 RESULT 1464
 ID AAY35078 standard; protein; 542 AA.
 DE Chlamydia pneumoniae protein not found in C. trachomatis.
 PN WO9927105-A2.
 PD 03-JUN-1999.
 PA (GEST) GENSET.
 Query Match 3.1%; Score 86.5; DB 2; Length 542;
 Best Local Similarity 19.9%; Pred. No. 27;
 RESULT 1465
 ID AAB61227 standard; protein; 591 AA.
 DE Mature human TANGO 325 protein.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 591;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1466
 ID ADB90765 standard; protein; 591 AA.
 DE Human TANGO 325 mature protein.
 PN US2003082586-A1.
 PD 01-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 7; Length 591;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1467
 ID ADF71500 standard; protein; 591 AA.
 DE Human TANGO 325 mature protein.
 PN US2003175733-A1.
 PD 18-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 7; Length 591;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1468
 ID ADM42025 standard; protein; 591 AA.
 DE Mature human TANGO 325.
 PN US2003170621-A1.
 PD 11-SEP-2003.
 PA (MCCA/) MCCARTHY S A.
 PA (FRAS/) FRASER C C.
 PA (SHAR/) SHARP J D.
 PA (BARN/) BARNES T M.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (WRIG/) WRIGHTON N.
 PA (GOOD/) GOODEARL A D J.
 PA (HOLT/) HOLTZMAN D A.
 PA (KHOD/) KHODADOUST M.
 Query Match 3.1%; Score 86.5; DB 7; Length 591;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1469
 ID ADI36907 standard; protein; 591 AA.
 DE Human LRR protein #2.

PN US2003220263-A1.
 PD 27-NOV-2003.
 PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 Query Match 3.1%; Score 86.5; DB 8; Length 591;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1470
 ID AAE06798 standard; protein; 597 AA.
 DE Mature human neuronal guidance molecule (NGM)-like protein #1.
 PN WO200157262-A1.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 597;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1471
 ID ADI36910 standard; protein; 597 AA.
 DE Human LRR protein #5.
 PN US2003220263-A1.
 PD 27-NOV-2003.
 PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 Query Match 3.1%; Score 86.5; DB 8; Length 597;
 Best Local Similarity 21.3%; Pred. No. 31;
 RESULT 1472
 ID ADS23090 standard; protein; 613 AA.
 DE Bacterial polypeptide #12123.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 3.1%; Score 86.5; DB 8; Length 613;
 Best Local Similarity 18.8%; Pred. No. 33;
 RESULT 1473
 ID AAB61225 standard; protein; 622 AA.
 DE Human TANGO 325 protein.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1474
 ID AAU12261 standard; protein; 622 AA.
 DE Human PRO4337 polypeptide sequence.
 PN WO200140466-A2.
 PD 07-JUN-2001.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 4; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1475
 ID AAU20531 standard; protein; 622 AA.
 DE Human secreted protein, Seq ID No 523.
 PN WO200155326-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 86.5; DB 4; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1476
ID AAB45703 standard; protein; 622 AA.
DE Human 7TM clone HDTIE58 protein fragment #1.
PN WO200071584-A1.
PD 30-NOV-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 86.5; DB 4; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1477
ID AAU19922 standard; protein; 622 AA.
DE Novel human calcium-binding protein #31.
PN WO200155304-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 86.5; DB 4; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1478
ID AAE06789 standard; protein; 622 AA.
DE Human neuronal guidance molecule (NGM)-like protein #1.
PN WO200157262-A1.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 86.5; DB 4; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1479
ID ABO17705 standard; protein; 622 AA.
DE Novel human secreted and transmembrane protein PRO4337.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1480
ID ABU80959 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1481
ID ABU66659 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1482
ID ABU59740 standard; protein; 622 AA.
DE Novel secreted and transmembrane protein PRO4337.
PN US2003017563-A1.
PD 23-JAN-2003.

PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1483
ID ABO24930 standard; protein; 622 AA.
DE Human secreted/transmembrane protein (PRO) #90.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1484
ID ABU66935 standard; protein; 622 AA.
DE Human secreted/transmembrane, PRO, protein SEQ ID 180.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1485
ID ADA45699 standard; protein; 622 AA.
DE Novel human secreted and transmembrane protein PRO4337.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1486
ID ADA76130 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1487
ID ADA18780 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1488
ID ADA61403 standard; protein; 622 AA.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1489
ID ADB19188 standard; protein; 622 AA.
DE Novel human secreted and transmembrane protein PRO4337.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1490
 ID ADB27729 standard; protein; 622 AA.
 DE Human PRO polypeptide #90.
 PN US2003082704-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1491
 ID ADA86208 standard; protein; 622 AA.
 DE Novel human secreted and transmembrane protein PRO4337.
 PN US2003082711-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1492
 ID ADB15772 standard; protein; 622 AA.
 DE Human PRO polypeptide #90.
 PN US2003087350-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1493
 ID ADA47558 standard; protein; 622 AA.
 DE Human PRO polypeptide #90.
 PN US2003073215-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1494
 ID ADA67353 standard; protein; 622 AA.
 DE Human PRO polypeptide #90.
 PN US2003068795-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1495
 ID ADB30360 standard; protein; 622 AA.
 DE Human PRO polypeptide #90.
 PN US2003068794-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;
 Best Local Similarity 21.3%; Pred. No. 33;
 RESULT 1496
 ID ADA85656 standard; protein; 622 AA.
 DE Novel human secreted and transmembrane protein PRO4337.
 PN US2003082693-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 3.1%; Score 86.5; DB 6; Length 622;

Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1497
ID ADA96868 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1498
ID ADA79172 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1499
ID ADA87311 standard; protein; 622 AA.
DE Novel human secreted and transmembrane protein PRO4337.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;
RESULT 1500
ID ADB16513 standard; protein; 622 AA.
DE Human PRO polypeptide #90.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 3.1%; Score 86.5; DB 6; Length 622;
Best Local Similarity 21.3%; Pred. No. 33;

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OM protein - protein search, using sw model

Run on: February 15, 2005, 09:44:27 ; Search time 43 Seconds
(without alignments)
907.941 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	679	24.5	533	4	US-09-949-016-5947	Sequence 5947, Ap
2	679	24.5	538	4	US-09-949-016-7684	Sequence 7684, Ap
3	674	24.3	533	5	PCT-US92-00282-3	Sequence 3, Appli
4	663.5	24.0	540	4	US-09-949-016-8465	Sequence 8465, Ap
5	663.5	24.0	540	4	US-09-949-016-9052	Sequence 9052, Ap
6	661.5	23.9	528	4	US-09-356-806-8	Sequence 8, Appli
7	658	23.8	531	5	PCT-US92-00282-6	Sequence 6, Appli
8	657	23.7	530	3	US-09-180-852-2	Sequence 2, Appli
9	651.5	23.5	524	4	US-09-356-806-40	Sequence 40, Appl
10	649	23.4	439	4	US-09-949-016-8605	Sequence 8605, Ap
11	649	23.4	530	4	US-09-356-806-113	Sequence 113, App

12	632.5	22.9	528	4	US-09-949-016-6999	Sequence 6999, Ap
13	629	22.7	531	5	PCT-US92-00282-5	Sequence 5, Appli
14	606	21.9	534	5	PCT-US92-00282-4	Sequence 4, Appli
15	600	21.7	529	5	PCT-US92-00282-7	Sequence 7, Appli
16	592.5	21.4	388	4	US-09-949-016-8466	Sequence 8466, Ap
17	592.5	21.4	388	4	US-09-949-016-8467	Sequence 8467, Ap
18	548	19.8	440	4	US-09-949-016-8606	Sequence 8606, Ap
19	548	19.8	440	4	US-09-949-016-8607	Sequence 8607, Ap
20	521	18.8	454	3	US-09-813-918-2	Sequence 2, Appli
21	521	18.8	454	4	US-10-060-311-2	Sequence 2, Appli
22	503.5	18.2	288	3	US-09-813-918-3	Sequence 3, Appli
23	503.5	18.2	288	4	US-10-060-311-3	Sequence 3, Appli
24	380	13.7	245	4	US-09-305-856B-18	Sequence 18, Appl
25	378.5	13.7	389	4	US-09-270-767-45357	Sequence 45357, A
26	360.5	13.0	256	4	US-09-270-767-33692	Sequence 33692, A
27	360.5	13.0	256	4	US-09-270-767-48909	Sequence 48909, A
28	346.5	12.5	515	3	US-08-942-012B-32	Sequence 32, Appl
29	342.5	12.4	460	3	US-08-942-012B-33	Sequence 33, Appl
30	321	11.6	515	3	US-08-942-012B-24	Sequence 24, Appl
31	316.5	11.4	488	3	US-08-942-012B-29	Sequence 29, Appl
32	316.5	11.4	488	3	US-08-942-012B-30	Sequence 30, Appl
33	300	10.8	288	4	US-09-305-856B-2	Sequence 2, Appli
34	300	10.8	288	5	PCT-US92-00282-19	Sequence 19, Appl
35	280	10.1	339	4	US-09-270-767-42493	Sequence 42493, A
36	272	9.8	493	3	US-08-942-012B-28	Sequence 28, Appl
37	259.5	9.4	489	3	US-08-942-012B-31	Sequence 31, Appl
38	258.5	9.3	287	4	US-09-305-856B-10	Sequence 10, Appl
39	256	9.2	310	4	US-09-305-856B-14	Sequence 14, Appl
40	255	9.2	289	4	US-09-305-856B-8	Sequence 8, Appli
41	252	9.1	286	5	PCT-US92-00282-9	Sequence 9, Appli
42	249	9.0	289	5	PCT-US92-00282-11	Sequence 11, Appl
43	248	9.0	506	3	US-08-942-012B-26	Sequence 26, Appl
44	246.5	8.9	506	3	US-08-942-012B-25	Sequence 25, Appl
45	246.5	8.9	506	6	5180581-2	Patent No. 5180581
46	246.5	8.9	506	6	5180581-2	Patent No. 5180581
47	244.5	8.8	289	4	US-09-305-856B-4	Sequence 4, Appli
48	244.5	8.8	289	5	PCT-US92-00282-15	Sequence 15, Appl
49	242	8.7	491	3	US-08-942-012B-27	Sequence 27, Appl
50	239	8.6	129	4	US-09-370-838-36	Sequence 36, Appl
51	239	8.6	129	4	US-09-854-133-36	Sequence 36, Appl
52	227	8.2	317	4	US-09-305-856B-12	Sequence 12, Appl
53	226	8.2	289	4	US-09-305-856B-6	Sequence 6, Appli
54	226	8.2	289	5	PCT-US92-00282-13	Sequence 13, Appl
55	223	8.1	253	4	US-09-305-856B-16	Sequence 16, Appl
56	214	7.7	52	2	US-08-466-583-7	Sequence 7, Appli
57	214	7.7	52	4	US-08-265-427-7	Sequence 7, Appli
58	214	7.7	52	5	PCT-US95-07820-7	Sequence 7, Appli
59	209.5	7.6	134	4	US-09-270-767-33090	Sequence 33090, A
60	209.5	7.6	134	4	US-09-270-767-48307	Sequence 48307, A
61	202	7.3	58	2	US-08-466-583-9	Sequence 9, Appli
62	202	7.3	58	4	US-08-265-427-9	Sequence 9, Appli
63	202	7.3	58	5	PCT-US95-07820-9	Sequence 9, Appli
64	198.5	7.2	322	4	US-09-270-767-42787	Sequence 42787, A
65	196	7.1	287	4	US-09-270-767-33212	Sequence 33212, A
66	192	6.9	135	4	US-09-270-767-45571	Sequence 45571, A
67	186.5	6.7	141	4	US-09-270-767-32085	Sequence 32085, A
68	176	6.4	463	4	US-08-311-731A-7	Sequence 7, Appli

69	175	6.3	56	2	US-08-466-583-4	Sequence 4, Appli
70	175	6.3	56	4	US-08-265-427-4	Sequence 4, Appli
71	175	6.3	56	5	PCT-US95-07820-4	Sequence 4, Appli
72	174	6.3	425	4	US-09-902-540-11331	Sequence 11331, A
73	173.5	6.3	303	4	US-09-270-767-41486	Sequence 41486, A
74	173.5	6.3	399	1	US-08-096-623A-20	Sequence 20, Appl
75	173.5	6.3	431	1	US-07-783-705A-2	Sequence 2, Appli
76	172.5	6.2	154	4	US-09-270-767-32580	Sequence 32580, A
77	172.5	6.2	154	4	US-09-270-767-47797	Sequence 47797, A
78	169.5	6.1	397	4	US-09-902-540-14631	Sequence 14631, A
79	168	6.1	74	5	PCT-US92-00282-24	Sequence 24, Appl
80	168	6.1	130	4	US-09-270-767-57790	Sequence 57790, A
81	167.5	6.1	397	4	US-09-724-797-26	Sequence 26, Appl
82	164	5.9	471	2	US-08-466-583-2	Sequence 2, Appli
83	164	5.9	471	4	US-08-265-427-2	Sequence 2, Appli
84	164	5.9	471	5	PCT-US95-07820-2	Sequence 2, Appli
85	162	5.9	459	4	US-09-679-263-4	Sequence 4, Appli
86	162	5.9	503	4	US-09-679-263-5	Sequence 5, Appli
87	161	5.8	454	4	US-09-679-263-12	Sequence 12, Appl
88	161	5.8	1198	4	US-09-284-768A-10	Sequence 10, Appl
89	160	5.8	473	4	US-09-284-768A-24	Sequence 24, Appl
90	159	5.7	63	2	US-08-466-583-8	Sequence 8, Appli
91	159	5.7	63	4	US-08-265-427-8	Sequence 8, Appli
92	159	5.7	63	5	PCT-US95-07820-8	Sequence 8, Appli
93	159	5.7	131	2	US-08-466-583-5	Sequence 5, Appli
94	159	5.7	131	4	US-08-265-427-5	Sequence 5, Appli
95	159	5.7	131	5	PCT-US95-07820-5	Sequence 5, Appli
96	158	5.7	190	4	US-09-615-192A-301	Sequence 301, App
97	157.5	5.7	131	2	US-08-466-583-6	Sequence 6, Appli
98	157.5	5.7	131	4	US-08-265-427-6	Sequence 6, Appli
99	157.5	5.7	131	5	PCT-US95-07820-6	Sequence 6, Appli
100	154	5.6	452	4	US-09-889-738-21	Sequence 21, Appl
101	153.5	5.5	452	4	US-08-311-731A-6	Sequence 6, Appli
102	149.5	5.4	414	1	US-09-337-913-1	Sequence 1, Appli
103	149.5	5.4	414	2	US-08-750-524-1	Sequence 1, Appli
104	147	5.3	185	4	US-09-270-767-56708	Sequence 56708, A
105	145.5	5.3	471	3	US-09-106-464-2	Sequence 2, Appli
106	142	5.1	78	4	US-09-513-999C-7361	Sequence 7361, Ap
107	139	5.0	476	4	US-09-673-300-10	Sequence 10, Appl
108	137	4.9	128	4	US-09-270-767-32549	Sequence 32549, A
109	136.5	4.9	488	2	US-08-797-226-2	Sequence 2, Appli
110	134	4.8	283	4	US-09-270-767-44687	Sequence 44687, A
111	134	4.8	488	4	US-09-673-300-8	Sequence 8, Appli
112	132.5	4.8	337	4	US-09-270-767-46773	Sequence 46773, A
113	131.5	4.8	419	4	US-09-724-797-95	Sequence 95, Appl
114	126.5	4.6	481	4	US-09-673-300-2	Sequence 2, Appli
115	120.5	4.4	422	4	US-09-679-279-17	Sequence 17, Appl
116	116.5	4.2	1114	2	US-08-576-626A-31	Sequence 31, Appl
117	114	4.1	2544	2	US-08-576-626A-32	Sequence 32, Appl
118	113	4.1	415	2	US-08-576-626A-52	Sequence 52, Appl
119	113	4.1	419	4	US-09-107-532A-4894	Sequence 4894, Ap
120	112.5	4.1	448	4	US-09-284-768A-23	Sequence 23, Appl
121	112.5	4.1	637	4	US-09-284-768A-20	Sequence 20, Appl
122	112.5	4.1	674	4	US-09-284-768A-21	Sequence 21, Appl
123	111	4.0	443	1	US-08-660-765A-4	Sequence 4, Appli
124	110.5	4.0	378	4	US-09-724-797-40	Sequence 40, Appl
125	109.5	4.0	652	4	US-09-489-039A-12461	Sequence 12461, A

126	109	3.9	408	2	US-08-924-847A-2	Sequence 2, Appli
127	109	3.9	408	3	US-09-120-052-2	Sequence 2, Appli
128	108	3.9	3079	5	PCT-US94-00198-4	Sequence 4, Appli
129	107	3.9	372	1	US-08-196-218-33	Sequence 33, Appl
130	107	3.9	372	1	US-08-681-953-33	Sequence 33, Appl
131	106.5	3.8	421	2	US-08-576-626A-53	Sequence 53, Appl
132	106	3.8	98	5	PCT-US92-00282-26	Sequence 26, Appl
133	105	3.8	408	2	US-08-926-258-2	Sequence 2, Appli
134	105	3.8	408	2	US-09-120-053-2	Sequence 2, Appli
135	105	3.8	408	3	US-09-198-212-2	Sequence 2, Appli
136	105	3.8	408	4	US-09-789-261-2	Sequence 2, Appli
137	104	3.8	417	4	US-09-679-279-11	Sequence 11, Appl
138	103.5	3.7	426	4	US-09-540-236-2053	Sequence 2053, Ap
139	103	3.7	967	3	US-09-139-802-201	Sequence 201, App
140	103	3.7	967	4	US-09-659-786-201	Sequence 201, App
141	101.5	3.7	436	4	US-09-679-279-4	Sequence 4, Appli
142	100	3.6	101	4	US-09-270-767-58100	Sequence 58100, A
143	100	3.6	388	4	US-09-602-787A-180	Sequence 180, App
144	100	3.6	455	3	US-09-036-987A-17	Sequence 17, Appl
145	100	3.6	455	3	US-09-370-700-17	Sequence 17, Appl
146	100	3.6	455	4	US-09-603-207-17	Sequence 17, Appl
147	98.5	3.6	391	3	US-09-134-001C-3952	Sequence 3952, Ap
148	98.5	3.6	834	1	US-07-977-434-8	Sequence 8, Appli
149	98.5	3.6	834	1	US-08-458-819-8	Sequence 8, Appli
150	98.5	3.6	834	5	PCT-US91-07035-8	Sequence 8, Appli
151	98	3.5	528	4	US-09-489-039A-13077	Sequence 13077, A
152	97.5	3.5	616	4	US-09-873-404-4	Sequence 4, Appli
153	97.5	3.5	616	4	US-10-243-735-4	Sequence 4, Appli
154	97.5	3.5	639	4	US-09-328-352-7786	Sequence 7786, Ap
155	96.5	3.5	608	4	US-09-284-768A-4	Sequence 4, Appli
156	96.5	3.5	991	4	US-09-248-796A-15239	Sequence 15239, A
157	96.5	3.5	1175	4	US-09-792-024-75	Sequence 75, Appl
158	95.5	3.5	1006	4	US-09-949-016-10730	Sequence 10730, A
159	95	3.4	72	4	US-09-270-767-61084	Sequence 61084, A
160	94.5	3.4	187	4	US-09-270-767-41857	Sequence 41857, A
161	94.5	3.4	605	4	US-09-248-796A-19205	Sequence 19205, A
162	94.5	3.4	705	4	US-09-198-452A-68	Sequence 68, Appl
163	94.5	3.4	705	4	US-09-438-185A-50	Sequence 50, Appl
164	94.5	3.4	838	4	US-09-758-282B-265	Sequence 265, App
165	94.5	3.4	838	4	US-09-577-304A-265	Sequence 265, App
166	94	3.4	1199	4	US-09-134-000C-5542	Sequence 5542, Ap
167	93.5	3.4	491	4	US-09-489-039A-12234	Sequence 12234, A
168	93.5	3.4	669	4	US-09-252-991A-31488	Sequence 31488, A
169	93.5	3.4	1837	4	US-09-438-185A-98	Sequence 98, Appl
170	92.5	3.3	460	1	US-08-351-981-4	Sequence 4, Appli
171	92	3.3	452	4	US-09-284-768A-22	Sequence 22, Appl
172	92	3.3	480	3	US-09-182-859-4	Sequence 4, Appli
173	92	3.3	480	3	US-09-170-670-5	Sequence 5, Appli
174	92	3.3	480	3	US-09-193-068-5	Sequence 5, Appli
175	92	3.3	480	3	US-09-183-412-5	Sequence 5, Appli
176	92	3.3	480	3	US-09-290-734-5	Sequence 5, Appli
177	92	3.3	480	4	US-09-672-459-4	Sequence 4, Appli
178	92	3.3	480	4	US-09-545-586-5	Sequence 5, Appli
179	92	3.3	480	4	US-10-186-042-4	Sequence 4, Appli
180	92	3.3	480	4	US-09-769-864-5	Sequence 5, Appli
181	92	3.3	483	2	US-08-600-908A-13	Sequence 13, Appl
182	92	3.3	483	3	US-08-683-838A-13	Sequence 13, Appl

183	92	3.3	483	3	US-09-291-023A-16	Sequence 16, Appl
184	92	3.3	483	4	US-09-537-168-6	Sequence 6, Appli
185	92	3.3	483	4	US-09-636-252A-13	Sequence 13, Appl
186	92	3.3	483	4	US-09-381-687-6	Sequence 6, Appli
187	92	3.3	483	4	US-09-540-715A-16	Sequence 16, Appl
188	92	3.3	514	1	US-08-720-899-4	Sequence 4, Appli
189	92	3.3	514	1	US-08-459-610-4	Sequence 4, Appli
190	92	3.3	514	2	US-08-343-804-4	Sequence 4, Appli
191	92	3.3	514	2	US-08-687-399-4	Sequence 4, Appli
192	92	3.3	514	2	US-08-600-908A-4	Sequence 4, Appli
193	92	3.3	514	3	US-08-683-838A-4	Sequence 4, Appli
194	92	3.3	514	3	US-09-264-097-4	Sequence 4, Appli
195	92	3.3	514	4	US-09-636-252A-4	Sequence 4, Appli
196	92	3.3	520	1	US-08-468-700-36	Sequence 36, Appl
197	92	3.3	520	1	US-08-645-971-4	Sequence 4, Appli
198	92	3.3	520	2	US-08-468-220-34	Sequence 34, Appl
199	92	3.3	520	2	US-08-468-698-34	Sequence 34, Appl
200	92	3.3	520	2	US-08-704-706A-36	Sequence 36, Appl
201	92	3.3	520	3	US-08-890-383-5	Sequence 5, Appli
202	92	3.3	520	3	US-08-914-679A-5	Sequence 5, Appli
203	92	3.3	520	3	US-08-985-659-37	Sequence 37, Appl
204	92	3.3	520	3	US-08-194-664A-34	Sequence 34, Appl
205	92	3.3	520	5	PCT-US94-01553A-34	Sequence 34, Appl
206	92	3.3	520	5	PCT-US95-10426-34	Sequence 34, Appl
207	92	3.3	657	4	US-09-284-768A-7	Sequence 7, Appli
208	92	3.3	817	4	US-09-248-796A-17089	Sequence 17089, A
209	91.5	3.3	143	4	US-09-270-767-62394	Sequence 62394, A
210	91	3.3	1826	4	US-09-198-452A-113	Sequence 113, App
211	90.5	3.3	727	4	US-09-543-681A-6690	Sequence 6690, Ap
212	90.5	3.3	1153	1	US-08-097-997A-14	Sequence 14, Appl
213	90	3.3	272	4	US-09-902-540-14018	Sequence 14018, A
214	90	3.3	366	3	US-09-134-001C-3198	Sequence 3198, Ap
215	90	3.3	620	4	US-09-861-451A-34	Sequence 34, Appl
216	89.5	3.2	471	4	US-09-051-961-7	Sequence 7, Appli
217	89	3.2	313	4	US-09-710-279-1216	Sequence 1216, Ap
218	89	3.2	357	4	US-09-710-279-410	Sequence 410, App
219	89	3.2	372	4	US-09-710-279-182	Sequence 182, App
220	88.5	3.2	197	4	US-09-270-767-32922	Sequence 32922, A
221	88.5	3.2	197	4	US-09-270-767-48139	Sequence 48139, A
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223	88.5	3.2	726	3	US-09-476-482-2	Sequence 2, Appli
224	88.5	3.2	726	3	US-09-517-605-6	Sequence 6, Appli
225	88	3.2	388	4	US-10-138-701-57	Sequence 57, Appl
226	88	3.2	540	4	US-09-248-796A-15935	Sequence 15935, A
227	88	3.2	745	4	US-09-543-681A-4267	Sequence 4267, Ap
228	88	3.2	838	4	US-09-758-282B-261	Sequence 261, App
229	88	3.2	838	4	US-09-577-304A-261	Sequence 261, App
230	88	3.2	1153	3	US-08-665-574C-14	Sequence 14, Appl
231	88	3.2	1153	3	US-08-946-994-14	Sequence 14, Appl
232	88	3.2	1153	4	US-09-963-137-202	Sequence 202, App
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234	87.5	3.2	729	4	US-09-949-016-10790	Sequence 10790, A
235	87.5	3.2	729	4	US-09-949-016-10791	Sequence 10791, A
236	87.5	3.2	1075	4	US-09-949-016-8308	Sequence 8308, Ap
237	87.5	3.2	1452	2	US-08-449-644-8	Sequence 8, Appli
238	87.5	3.2	1452	2	US-08-087-244A-8	Sequence 8, Appli
239	87	3.1	565	2	US-08-357-533A-9	Sequence 9, Appli

240	87	3.1	565	2	US-08-459-009-9	Sequence 9, Appli
241	87	3.1	565	3	US-08-459-951-9	Sequence 9, Appli
242	87	3.1	944	4	US-09-107-532A-4864	Sequence 4864, Ap
243	86.5	3.1	542	4	US-09-198-452A-496	Sequence 496, App
244	86.5	3.1	696	4	US-09-438-185A-464	Sequence 464, App
245	86.5	3.1	908	4	US-09-623-326-9	Sequence 9, Appli
246	86.5	3.1	1022	1	US-08-271-364A-8	Sequence 8, Appli
247	86.5	3.1	1022	2	US-08-222-715B-27	Sequence 27, Appl
248	86.5	3.1	1060	4	US-09-248-796A-16624	Sequence 16624, A
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251	86	3.1	197	4	US-10-060-311-4	Sequence 4, Appli
252	86	3.1	268	4	US-09-371-338-21	Sequence 21, Appl
253	86	3.1	355	4	US-09-501-115-12	Sequence 12, Appl
254	86	3.1	364	4	US-09-583-110-5235	Sequence 5235, Ap
255	86	3.1	690	4	US-09-371-338-19	Sequence 19, Appl
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258	85.5	3.1	352	4	US-09-583-110-2857	Sequence 2857, Ap
259	85.5	3.1	355	4	US-09-107-433-4605	Sequence 4605, Ap
260	85.5	3.1	389	4	US-09-134-000C-5382	Sequence 5382, Ap
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262	85.5	3.1	494	3	US-08-988-251-2	Sequence 2, Appli
263	85.5	3.1	494	3	US-09-386-048-2	Sequence 2, Appli
264	85.5	3.1	617	4	US-09-252-991A-29507	Sequence 29507, A
265	85.5	3.1	658	3	US-08-953-040-9	Sequence 9, Appli
266	85.5	3.1	898	4	US-09-489-039A-10322	Sequence 10322, A
267	85.5	3.1	930	3	US-08-953-040-2	Sequence 2, Appli
268	85.5	3.1	930	4	US-09-583-110-3208	Sequence 3208, Ap
269	85.5	3.1	939	4	US-09-107-433-4543	Sequence 4543, Ap
270	85	3.1	893	1	US-07-977-434-4	Sequence 4, Appli
271	85	3.1	893	1	US-08-458-819-4	Sequence 4, Appli
272	85	3.1	893	3	US-09-105-697-10	Sequence 10, Appl
273	85	3.1	893	3	US-09-514-302-4	Sequence 4, Appli
274	85	3.1	893	4	US-09-623-326-18	Sequence 18, Appl
275	85	3.1	893	4	US-10-014-436-4	Sequence 4, Appli
276	85	3.1	893	5	PCT-US91-07035-4	Sequence 4, Appli
277	85	3.1	1247	4	US-09-134-000C-4968	Sequence 4968, Ap
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283	85	3.1	1719	3	US-09-586-472-4	Sequence 4, Appli
284	85	3.1	1719	4	US-09-528-706-4	Sequence 4, Appli
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286	85	3.1	1938	4	US-10-014-436-2	Sequence 2, Appli
287	84.5	3.1	319	1	US-08-597-236-7	Sequence 7, Appli
288	84.5	3.1	319	1	US-08-746-682A-7	Sequence 7, Appli
289	84.5	3.1	447	3	US-09-305-001-2	Sequence 2, Appli
290	84.5	3.1	447	4	US-09-583-110-3287	Sequence 3287, Ap
291	84.5	3.1	451	4	US-09-107-433-3636	Sequence 3636, Ap
292	84.5	3.1	471	4	US-09-538-092-938	Sequence 938, App
293	84.5	3.1	481	4	US-09-673-395A-277	Sequence 277, App
294	84.5	3.1	489	4	US-09-949-016-7030	Sequence 7030, Ap
295	84.5	3.1	492	3	US-08-984-618-2	Sequence 2, Appli
296	84.5	3.1	635	4	US-10-101-464A-932	Sequence 932, App

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300	84.5	3.1	1452	2	US-08-991-258A-4	Sequence 4, Appli
301	84.5	3.1	1452	2	US-08-769-399-4	Sequence 4, Appli
302	84.5	3.1	1452	3	US-08-991-953A-4	Sequence 4, Appli
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306	83.5	3.0	431	2	US-08-576-626A-54	Sequence 54, Appl
307	83.5	3.0	460	4	US-09-248-796A-14306	Sequence 14306, A
308	83.5	3.0	499	4	US-09-270-767-57610	Sequence 57610, A
309	83.5	3.0	644	4	US-09-198-452A-785	Sequence 785, App
310	83.5	3.0	716	4	US-09-270-767-42322	Sequence 42322, A
311	83.5	3.0	717	4	US-09-949-016-5999	Sequence 5999, Ap
312	83.5	3.0	2644	4	US-09-029-047C-2	Sequence 2, Appli
313	83	3.0	271	4	US-09-252-991A-21522	Sequence 21522, A
314	83	3.0	318	4	US-09-328-352-7247	Sequence 7247, Ap
315	83	3.0	360	4	US-09-501-115-4	Sequence 4, Appli
316	83	3.0	418	3	US-08-855-910-11	Sequence 11, Appl
317	83	3.0	433	4	US-09-134-000C-3686	Sequence 3686, Ap
318	83	3.0	607	4	US-09-344-882-18	Sequence 18, Appl
319	83	3.0	842	4	US-09-758-282B-241	Sequence 241, App
320	83	3.0	842	4	US-09-577-304A-241	Sequence 241, App
321	83	3.0	3169	2	US-08-477-451-6	Sequence 6, Appli
322	82.5	3.0	415	4	US-09-949-016-10838	Sequence 10838, A
323	82.5	3.0	445	4	US-09-252-991A-17629	Sequence 17629, A
324	82.5	3.0	471	4	US-09-670-216-31	Sequence 31, Appl
325	82.5	3.0	472	4	US-09-270-767-58032	Sequence 58032, A
326	82.5	3.0	573	3	US-09-134-001C-4942	Sequence 4942, Ap
327	82.5	3.0	604	4	US-09-508-213-3	Sequence 3, Appli
328	82.5	3.0	625	4	US-09-270-767-42712	Sequence 42712, A
329	82.5	3.0	704	4	US-09-543-681A-7274	Sequence 7274, Ap
330	82.5	3.0	819	3	US-09-511-625B-4	Sequence 4, Appli
331	82.5	3.0	832	4	US-09-758-282B-268	Sequence 268, App
332	82.5	3.0	832	4	US-09-577-304A-268	Sequence 268, App
333	82.5	3.0	847	1	US-08-276-099A-2	Sequence 2, Appli
334	82.5	3.0	847	1	US-08-781-890-2	Sequence 2, Appli
335	82.5	3.0	847	3	US-09-087-465-12	Sequence 12, Appl
336	82.5	3.0	847	4	US-09-972-800A-10	Sequence 10, Appl
337	82.5	3.0	1226	4	US-09-601-537-7	Sequence 7, Appli
338	82.5	3.0	1227	2	US-08-760-075A-18	Sequence 18, Appl
339	82.5	3.0	1227	3	US-09-338-546-18	Sequence 18, Appl
340	82.5	3.0	1227	4	US-09-659-084-18	Sequence 18, Appl
341	82.5	3.0	1256	4	US-09-949-016-9991	Sequence 9991, Ap
342	82.5	3.0	1534	4	US-09-543-681A-5182	Sequence 5182, Ap
343	82.5	3.0	3782	3	US-09-105-537-4	Sequence 4, Appli
344	82	3.0	312	4	US-09-107-532A-4376	Sequence 4376, Ap
345	82	3.0	390	4	US-09-543-681A-7466	Sequence 7466, Ap
346	82	3.0	397	4	US-09-660-107-1	Sequence 1, Appli
347	82	3.0	397	6	5457090-2	Patent No. 5457090
348	82	3.0	397	6	5495001-7	Patent No. 5495001
349	82	3.0	397	6	5457090-2	Patent No. 5457090
350	82	3.0	397	6	5495001-7	Patent No. 5495001
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352	82	3.0	545	4	US-09-801-774-1	Sequence 1, Appli
353	82	3.0	589	4	US-09-543-681A-4194	Sequence 4194, Ap

354	82	3.0	834	4	US-09-334-818A-2	Sequence 2, Appli
355	82	3.0	842	4	US-09-758-282B-77	Sequence 77, Appl
356	82	3.0	842	4	US-09-758-282B-93	Sequence 93, Appl
357	82	3.0	842	4	US-09-577-304A-77	Sequence 77, Appl
358	82	3.0	842	4	US-09-577-304A-93	Sequence 93, Appl
359	82	3.0	884	4	US-09-543-681A-5437	Sequence 5437, Ap
360	82	3.0	912	4	US-09-248-796A-20032	Sequence 20032, A
361	82	3.0	959	4	US-09-107-433-4334	Sequence 4334, Ap
362	82	3.0	1032	4	US-09-583-110-3366	Sequence 3366, Ap
363	82	3.0	1096	4	US-09-438-185A-739	Sequence 739, App
364	81.5	2.9	492	1	US-10-095-946-2	Sequence 2, Appli
365	81.5	2.9	492	3	US-09-183-959-2	Sequence 2, Appli
366	81.5	2.9	492	4	US-09-347-650-14	Sequence 14, Appl
367	81.5	2.9	492	4	US-09-535-315-2	Sequence 2, Appli
368	81.5	2.9	648	4	US-09-252-991A-24628	Sequence 24628, A
369	81.5	2.9	717	4	US-09-710-279-3022	Sequence 3022, Ap
370	81.5	2.9	901	4	US-09-710-279-342	Sequence 342, App
371	81	2.9	380	4	US-09-252-991A-28929	Sequence 28929, A
372	81	2.9	503	4	US-09-144-367-2	Sequence 2, Appli
373	81	2.9	536	4	US-09-248-796A-19182	Sequence 19182, A
374	81	2.9	610	3	US-08-656-664-54	Sequence 54, Appl
375	81	2.9	610	5	PCT-US96-09641-54	Sequence 54, Appl
376	81	2.9	694	4	US-09-583-110-4272	Sequence 4272, Ap
377	81	2.9	805	4	US-09-598-401C-77	Sequence 77, Appl
378	81	2.9	807	4	US-09-538-092-574	Sequence 574, App
379	81	2.9	834	3	US-08-539-205A-6	Sequence 6, Appli
380	81	2.9	834	4	US-09-392-163A-6	Sequence 6, Appli
381	81	2.9	1024	3	US-09-091-117-5	Sequence 5, Appli
382	81	2.9	1042	4	US-09-512-250C-32	Sequence 32, Appl
383	80.5	2.9	499	3	US-09-457-040B-13	Sequence 13, Appl
384	80.5	2.9	813	4	US-09-328-352-7421	Sequence 7421, Ap
385	80.5	2.9	832	4	US-09-758-282B-251	Sequence 251, App
386	80.5	2.9	832	4	US-09-577-304A-251	Sequence 251, App
387	80.5	2.9	1072	4	US-09-248-796A-16400	Sequence 16400, A
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389	80	2.9	342	4	US-09-248-796A-16595	Sequence 16595, A
390	80	2.9	378	4	US-09-107-532A-6756	Sequence 6756, Ap
391	80	2.9	512	4	US-09-107-532A-5262	Sequence 5262, Ap
392	80	2.9	789	3	US-08-727-308-1	Sequence 1, Appli
393	80	2.9	1627	4	US-09-252-991A-28697	Sequence 28697, A
394	80	2.9	2108	4	US-09-538-092-87	Sequence 87, Appl
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396	79.5	2.9	353	4	US-09-248-796A-15118	Sequence 15118, A
397	79.5	2.9	366	4	US-09-359-268A-27	Sequence 27, Appl
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399	79.5	2.9	369	2	US-09-165-234-8....	Sequence 8, Appli
400	79.5	2.9	369	3	US-09-274-570-8	Sequence 8, Appli
401	79.5	2.9	418	4	US-09-248-796A-17723	Sequence 17723, A
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403	79.5	2.9	446	3	US-08-879-941-2	Sequence 2, Appli
404	79.5	2.9	446	3	US-09-747-116-2	Sequence 2, Appli
405	79.5	2.9	463	4	US-09-107-433-3506	Sequence 3506, Ap
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407	79.5	2.9	519	4	US-09-252-991A-16737	Sequence 16737, A
408	79.5	2.9	525	1	US-08-077-939-15	Sequence 15, Appl
409	79.5	2.9	525	1	US-08-461-599-15	Sequence 15, Appl
410	79.5	2.9	525	1	US-08-461-621-15	Sequence 15, Appl

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412	79.5	2.9	676	4	US-09-107-532A-6028	Sequence 6028, Ap
413	79.5	2.9	800	4	US-09-248-796A-16801	Sequence 16801, A
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416	79.5	2.9	885	3	US-08-841-089-2	Sequence 2, Appli
417	79.5	2.9	885	3	US-09-301-085-2	Sequence 2, Appli
418	79.5	2.9	885	5	PCT-US95-04570-2	Sequence 2, Appli
419	79.5	2.9	885	5	PCT-US95-04589-2	Sequence 2, Appli
420	79.5	2.9	907	3	US-08-930-996A-7	Sequence 7, Appli
421	79.5	2.9	909	2	US-08-310-912A-142	Sequence 142, App
422	79.5	2.9	909	3	US-09-301-085-142	Sequence 142, App
423	79.5	2.9	909	5	PCT-US95-04589-142	Sequence 142, App
424	79.5	2.9	942	4	US-09-657-931A-9	Sequence 9, Appli
425	79	2.9	233	4	US-09-248-796A-14148	Sequence 14148, A
426	79	2.9	432	4	US-09-949-016-6747	Sequence 6747, Ap
427	79	2.9	490	4	US-09-800-170-23	Sequence 23, Appl
428	79	2.9	494	3	US-08-484-661A-39	Sequence 39, Appl
429	79	2.9	494	3	US-08-656-664-39	Sequence 39, Appl
430	79	2.9	494	5	PCT-US96-09641-39	Sequence 39, Appl
431	79	2.9	571	3	US-08-484-661A-37	Sequence 37, Appl
432	79	2.9	571	3	US-08-656-664-37	Sequence 37, Appl
433	79	2.9	571	5	PCT-US96-09641-37	Sequence 37, Appl
434	79	2.9	578	3	US-08-484-661A-11	Sequence 11, Appl
435	79	2.9	578	3	US-08-656-664-11	Sequence 11, Appl
436	79	2.9	578	5	PCT-US96-09641-11	Sequence 11, Appl
437	79	2.9	581	4	US-09-248-796A-20657	Sequence 20657, A
438	79	2.9	607	4	US-09-344-882-16	Sequence 16, Appl
439	79	2.9	610	3	US-08-484-661A-8	Sequence 8, Appli
440	79	2.9	610	3	US-08-484-661A-16	Sequence 16, Appl
441	79	2.9	610	3	US-08-484-661A-19	Sequence 19, Appl
442	79	2.9	610	3	US-08-484-661A-23	Sequence 23, Appl
443	79	2.9	610	3	US-08-484-661A-26	Sequence 26, Appl
444	79	2.9	610	3	US-08-484-661A-29	Sequence 29, Appl
445	79	2.9	610	3	US-08-484-661A-33	Sequence 33, Appl
446	79	2.9	610	3	US-08-484-661A-35	Sequence 35, Appl
447	79	2.9	610	3	US-08-656-664-8	Sequence 8, Appli
448	79	2.9	610	3	US-08-656-664-16	Sequence 16, Appl
449	79	2.9	610	3	US-08-656-664-19	Sequence 19, Appl
450	79	2.9	610	3	US-08-656-664-23	Sequence 23, Appl
451	79	2.9	610	3	US-08-656-664-26	Sequence 26, Appl
452	79	2.9	610	3	US-08-656-664-29	Sequence 29, Appl
453	79	2.9	610	3	US-08-656-664-33	Sequence 33, Appl
454	79	2.9	610	3	US-08-656-664-35	Sequence 35, Appl
455	79	2.9	610	3	US-09-019-160-4	Sequence 4, Appli
456	79	2.9	610	5	PCT-US96-09641-8	Sequence 8, Appli
457	79	2.9	610	5	PCT-US96-09641-16	Sequence 16, Appl
458	79	2.9	610	5	PCT-US96-09641-19	Sequence 19, Appl
459	79	2.9	610	5	PCT-US96-09641-23	Sequence 23, Appl
460	79	2.9	610	5	PCT-US96-09641-26	Sequence 26, Appl
461	79	2.9	610	5	PCT-US96-09641-29	Sequence 29, Appl
462	79	2.9	610	5	PCT-US96-09641-33	Sequence 33, Appl
463	79	2.9	610	5	PCT-US96-09641-35	Sequence 35, Appl
464	79	2.9	677	3	US-09-019-160-3	Sequence 3, Appli
465	79	2.9	684	4	US-09-489-039A-13496	Sequence 13496, A
466	79	2.9	699	4	US-09-438-185A-506	Sequence 506, App
467	79	2.9	708	3	US-09-019-160-5	Sequence 5, Appli

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469	79	2.9	861	3	US-08-977-221-67	Sequence 67, Appl
470	79	2.9	861	4	US-09-483-831B-67	Sequence 67, Appl
471	79	2.9	861	5	PCT-US95-06613-67	Sequence 67, Appl
472	79	2.9	893	3	US-08-484-661A-2	Sequence 2, Appli
473	79	2.9	893	3	US-08-656-664-2	Sequence 2, Appli
474	79	2.9	893	3	US-09-019-160-2	Sequence 2, Appli
475	79	2.9	893	3	US-09-019-160-6	Sequence 6, Appli
476	79	2.9	893	3	US-09-019-160-7	Sequence 7, Appli
477	79	2.9	893	3	US-09-019-160-8	Sequence 8, Appli
478	79	2.9	893	3	US-09-019-160-9	Sequence 9, Appli
479	79	2.9	893	5	PCT-US96-09641-2	Sequence 2, Appli
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481	79	2.9	986	4	US-08-311-731A-2	Sequence 2, Appli
482	79	2.9	1271	1	US-08-095-734-2	Sequence 2, Appli
483	79	2.9	1271	2	US-08-444-623-2	Sequence 2, Appli
484	79	2.9	1271	3	US-08-471-869-2	Sequence 2, Appli
485	79	2.9	1271	3	US-09-342-563-2	Sequence 2, Appli
486	79	2.9	1271	5	PCT-US94-08267-2	Sequence 2, Appli
487	79	2.9	2080	4	US-09-382-552-2	Sequence 2, Appli
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490	78.5	2.8	467	3	US-09-391-958-3	Sequence 3, Appli
491	78.5	2.8	480	2	US-08-724-394A-9	Sequence 9, Appli
492	78.5	2.8	500	3	US-09-134-001C-3990	Sequence 3990, Ap
493	78.5	2.8	515	4	US-09-869-433-2	Sequence 2, Appli
494	78.5	2.8	567	4	US-09-543-681A-5673	Sequence 5673, Ap
495	78.5	2.8	682	4	US-09-252-991A-31897	Sequence 31897, A
496	78.5	2.8	770	4	US-09-248-796A-17215	Sequence 17215, A
497	78.5	2.8	816	4	US-09-543-681A-7118	Sequence 7118, Ap
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500	78	2.8	218	4	US-09-327-983-6	Sequence 6, Appli
501	78	2.8	336	4	US-09-134-000C-6236	Sequence 6236, Ap
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505	78	2.8	416	4	US-09-568-189A-61	Sequence 61, Appl
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508	78	2.8	426	3	US-09-105-537-20	Sequence 20, Appl
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510	78	2.8	426	4	US-09-657-440-8	Sequence 8, Appli
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514	78	2.8	474	3	US-09-584-628-2	Sequence 2, Appli
515	78	2.8	477	3	US-08-772-270A-13	Sequence 13, Appl
516	78	2.8	508	4	US-09-949-016-7092	Sequence 7092, Ap
517	78	2.8	508	4	US-09-949-016-8562	Sequence 8562, Ap
518	78	2.8	532	4	US-09-270-767-46234	Sequence 46234, A
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520	78	2.8	654	3	US-09-134-001C-3261	Sequence 3261, Ap
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522	78	2.8	700	2	US-08-487-826B-10	Sequence 10, Appl
523	78	2.8	700	3	US-09-210-288-10	Sequence 10, Appl
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527	78	2.8	876	3	US-09-012-872-2	Sequence 2, Appli
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529	78	2.8	974	4	US-10-101-464A-921	Sequence 921, App
530	78	2.8	1077	4	US-09-397-550-24	Sequence 24, Appl
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532	78	2.8	1122	4	US-09-711-164-451	Sequence 451, App
533	78	2.8	1467	4	US-09-134-000C-6740	Sequence 6740, Ap
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535	78	2.8	1706	2	US-08-399-411-2	Sequence 2, Appli
536	78	2.8	1706	3	US-08-516-859A-2	Sequence 2, Appli
537	78	2.8	1706	3	US-09-586-472-2	Sequence 2, Appli
538	78	2.8	1706	4	US-09-528-706-2	Sequence 2, Appli
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546	78	2.8	3959	3	US-09-407-562-30	Sequence 30, Appl
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548	77.5	2.8	245	4	US-09-270-767-46576	Sequence 46576, A
549	77.5	2.8	356	4	US-09-302-626B-56	Sequence 56, Appl
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553	77.5	2.8	498	4	US-09-328-352-5006	Sequence 5006, Ap
554	77.5	2.8	512	4	US-10-142-231-66	Sequence 66, Appl
555	77.5	2.8	576	1	US-08-221-817-22	Sequence 22, Appl
556	77.5	2.8	576	1	US-08-454-439-22	Sequence 22, Appl
557	77.5	2.8	576	5	PCT-US94-10487-22	Sequence 22, Appl
558	77.5	2.8	589	4	US-09-248-796A-19246	Sequence 19246, A
559	77.5	2.8	628	4	US-09-345-473E-48	Sequence 48, Appl
560	77.5	2.8	659	4	US-09-583-110-3110	Sequence 3110, Ap
561	77.5	2.8	751	4	US-09-252-991A-25481	Sequence 25481, A
562	77.5	2.8	765	3	US-09-134-001C-3681	Sequence 3681, Ap
563	77.5	2.8	810	4	US-09-328-352-7181	Sequence 7181, Ap
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565	77.5	2.8	893	3	US-08-706-706-3	Sequence 3, Appli
566	77.5	2.8	893	4	US-09-238-471-3	Sequence 3, Appli
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568	77.5	2.8	1278	4	US-09-462-136-2	Sequence 2, Appli
569	77.5	2.8	1318	4	US-09-949-016-10152	Sequence 10152, A
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571	77	2.8	294	4	US-09-583-110-3740	Sequence 3740, Ap
572	77	2.8	307	4	US-09-710-279-2668	Sequence 2668, Ap
573	77	2.8	315	4	US-09-107-433-3121	Sequence 3121, Ap
574	77	2.8	319	3	US-09-134-001C-5553	Sequence 5553, Ap
575	77	2.8	358	4	US-09-710-279-2136	Sequence 2136, Ap
576	77	2.8	365	4	US-09-710-279-470	Sequence 470, App
577	77	2.8	366	3	US-09-134-001C-5502	Sequence 5502, Ap
578	77	2.8	390	3	US-09-036-987A-8	Sequence 8, Appli
579	77	2.8	390	3	US-09-370-700-8	Sequence 8, Appli
580	77	2.8	390	4	US-09-603-207-8	Sequence 8, Appli
581	77	2.8	392	4	US-09-489-039A-11256	Sequence 11256, A

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583	77	2.8	449	4	US-09-530-838-6	Sequence 6, Appli
584	77	2.8	480	4	US-09-543-681A-4532	Sequence 4532, Ap
585	77	2.8	593	4	US-09-489-039A-8609	Sequence 8609, Ap
586	77	2.8	610	3	US-09-019-160-10	Sequence 10, Appl
587	77	2.8	614	4	US-09-328-352-5476	Sequence 5476, Ap
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589	77	2.8	646	4	US-09-248-796A-20617	Sequence 20617, A
590	77	2.8	651	4	US-09-583-110-3943	Sequence 3943, Ap
591	77	2.8	663	4	US-09-107-433-4766	Sequence 4766, Ap
592	77	2.8	683	4	US-09-591-095-6	Sequence 6, Appli
593	77	2.8	690	4	US-09-540-236-3507	Sequence 3507, Ap
594	77	2.8	743	4	US-09-248-796A-15523	Sequence 15523, A
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596	77	2.8	793	4	US-09-280-597-3	Sequence 3, Appli
597	77	2.8	988	4	US-09-252-991A-27246	Sequence 27246, A
598	77	2.8	1441	4	US-09-949-016-10397	Sequence 10397, A
599	77	2.8	2210	4	US-09-309-572-7	Sequence 7, Appli
600	77	2.8	2210	4	US-09-718-096-7	Sequence 7, Appli
601	77	2.8	2787	3	US-09-245-041-15	Sequence 15, Appl
602	77	2.8	2787	4	US-09-358-055B-15	Sequence 15, Appl
603	77	2.8	2787	4	US-09-893-238-15	Sequence 15, Appl
604	76.5	2.8	355	4	US-09-248-796A-16878	Sequence 16878, A
605	76.5	2.8	358	4	US-09-198-452A-1049	Sequence 1049, Ap
606	76.5	2.8	358	4	US-09-438-185A-978	Sequence 978, App
607	76.5	2.8	372	2	US-08-884-681-1	Sequence 1, Appli
608	76.5	2.8	372	3	US-09-258-643-1	Sequence 1, Appli
609	76.5	2.8	426	1	US-08-455-550-21	Sequence 21, Appl
610	76.5	2.8	525	1	US-08-077-939-17	Sequence 17, Appl
611	76.5	2.8	525	1	US-08-461-599-17	Sequence 17, Appl
612	76.5	2.8	525	1	US-08-461-621-17	Sequence 17, Appl
613	76.5	2.8	525	1	US-08-465-334-17	Sequence 17, Appl
614	76.5	2.8	547	4	US-09-248-796A-18204	Sequence 18204, A
615	76.5	2.8	619	3	US-09-156-253-48	Sequence 48, Appl
616	76.5	2.8	619	5	PCT-US93-03027-6	Sequence 6, Appli
617	76.5	2.8	630	4	US-09-248-796A-19619	Sequence 19619, A
618	76.5	2.8	681	4	US-09-248-796A-17348	Sequence 17348, A
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621	76.5	2.8	892	1	US-08-458-819-12	Sequence 12, Appl
622	76.5	2.8	892	5	PCT-US91-07035-12	Sequence 12, Appl
623	76.5	2.8	1019	4	US-09-252-991A-24417	Sequence 24417, A
624	76.5	2.8	1030	3	US-09-091-117-2	Sequence 2, Appli
625	76.5	2.8	1286	3	US-09-268-140-3	Sequence 3, Appli
626	76.5	2.8	1447	3	US-09-376-330-17	Sequence 17, Appl
627	76	2.7	206	4	US-09-328-352-4683	Sequence 4683, Ap
628	76	2.7	279	4	US-09-134-000C-6430	Sequence 6430, Ap
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631	76	2.7	397	6	5187089-10	Patent No. 5187089
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633	76	2.7	448	3	US-09-351-497-2	Sequence 2, Appli
634	76	2.7	448	4	US-09-270-767-42145	Sequence 42145, A
635	76	2.7	482	4	US-10-196-927-4	Sequence 4, Appli
636	76	2.7	553	4	US-09-248-796A-19257	Sequence 19257, A
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638	76	2.7	675	4	US-09-248-796A-20699	Sequence 20699, A

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641	76	2.7	714	4	US-09-438-185A-289	Sequence 289, App
642	76	2.7	741	4	US-09-328-352-5898	Sequence 5898, Ap
643	76	2.7	1083	3	US-08-895-601-5	Sequence 5, Appli
644	76	2.7	1240	3	US-08-930-996A-4	Sequence 4, Appli
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646	76	2.7	2008	4	US-09-270-767-46774	Sequence 46774, A
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648	75.5	2.7	249	2	US-09-144-925-8	Sequence 8, Appli
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650	75.5	2.7	289	4	US-09-270-767-51843	Sequence 51843, A
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652	75.5	2.7	414	2	US-08-845-161A-2	Sequence 2, Appli
653	75.5	2.7	414	3	US-09-270-751-2	Sequence 2, Appli
654	75.5	2.7	414	4	US-09-168-218B-4	Sequence 4, Appli
655	75.5	2.7	445	4	US-10-067-977-2	Sequence 2, Appli
656	75.5	2.7	490	4	US-09-134-000C-5122	Sequence 5122, Ap
657	75.5	2.7	502	4	US-09-417-704-1	Sequence 1, Appli
658	75.5	2.7	509	4	US-09-494-297A-5	Sequence 5, Appli
659	75.5	2.7	510	4	US-10-029-180-94	Sequence 94, Appl
660	75.5	2.7	519	4	US-09-198-452A-561	Sequence 561, App
661	75.5	2.7	521	4	US-09-438-185A-523	Sequence 523, App
662	75.5	2.7	524	4	US-09-198-452A-369	Sequence 369, App
663	75.5	2.7	524	4	US-09-438-185A-353	Sequence 353, App
664	75.5	2.7	543	4	US-09-107-532A-5041	Sequence 5041, Ap
665	75.5	2.7	739	4	US-09-248-796A-19328	Sequence 19328, A
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667	75.5	2.7	834	1	US-08-073-384C-6	Sequence 6, Appli
668	75.5	2.7	834	1	US-08-254-359A-6	Sequence 6, Appli
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670	75.5	2.7	834	1	US-08-483-043-6	Sequence 6, Appli
671	75.5	2.7	834	1	US-08-459-383-31	Sequence 31, Appl
672	75.5	2.7	834	1	US-08-458-819-10	Sequence 10, Appl
673	75.5	2.7	834	1	US-08-481-238-6	Sequence 6, Appli
674	75.5	2.7	834	2	US-08-471-066B-6	Sequence 6, Appli
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676	75.5	2.7	834	2	US-08-757-653-6	Sequence 6, Appli
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678	75.5	2.7	834	2	US-08-756-386-6	Sequence 6, Appli
679	75.5	2.7	834	2	US-08-823-516-6	Sequence 6, Appli
680	75.5	2.7	834	3	US-08-682-853A-6	Sequence 6, Appli
681	75.5	2.7	834	3	US-08-759-038-6	Sequence 6, Appli
682	75.5	2.7	834	3	US-08-758-314-6	Sequence 6, Appli
683	75.5	2.7	834	3	US-09-350-309-6	Sequence 6, Appli
684	75.5	2.7	834	3	US-08-520-946-6	Sequence 6, Appli
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686	75.5	2.7	834	4	US-09-308-825A-6	Sequence 6, Appli
687	75.5	2.7	834	4	US-09-758-282B-267	Sequence 267, App
688	75.5	2.7	834	4	US-09-655-378A-6	Sequence 6, Appli
689	75.5	2.7	834	4	US-09-940-244-6	Sequence 6, Appli
690	75.5	2.7	834	4	US-09-333-145-6	Sequence 6, Appli
691	75.5	2.7	834	4	US-09-577-304A-267	Sequence 267, App
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694	75.5	2.7	838	4	US-09-132-316-3	Sequence 3, Appli
695	75.5	2.7	838	4	US-09-667-422-9	Sequence 9, Appli

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697	75.5	2.7	842	4	US-09-758-282B-72	Sequence 72, Appl
698	75.5	2.7	842	4	US-09-758-282B-91	Sequence 91, Appl
699	75.5	2.7	842	4	US-09-758-282B-160	Sequence 160, App
700	75.5	2.7	842	4	US-09-758-282B-163	Sequence 163, App
701	75.5	2.7	842	4	US-09-758-282B-166	Sequence 166, App
702	75.5	2.7	842	4	US-09-758-282B-212	Sequence 212, App
703	75.5	2.7	842	4	US-09-758-282B-214	Sequence 214, App
704	75.5	2.7	842	4	US-09-758-282B-216	Sequence 216, App
705	75.5	2.7	842	4	US-09-577-304A-72	Sequence 72, Appl
706	75.5	2.7	842	4	US-09-577-304A-91	Sequence 91, Appl
707	75.5	2.7	842	4	US-09-577-304A-160	Sequence 160, App
708	75.5	2.7	842	4	US-09-577-304A-163	Sequence 163, App
709	75.5	2.7	842	4	US-09-577-304A-166	Sequence 166, App
710	75.5	2.7	842	4	US-09-577-304A-212	Sequence 212, App
711	75.5	2.7	842	4	US-09-577-304A-214	Sequence 214, App
712	75.5	2.7	842	4	US-09-577-304A-216	Sequence 216, App
713	75.5	2.7	842	4	US-09-777-430C-20	Sequence 20, Appl
714	75.5	2.7	842	4	US-09-777-430C-23	Sequence 23, Appl
715	75.5	2.7	842	4	US-09-777-430C-26	Sequence 26, Appl
716	75.5	2.7	915	1	US-08-346-455B-69	Sequence 69, Appl
717	75.5	2.7	915	3	US-08-977-221-69	Sequence 69, Appl
718	75.5	2.7	915	4	US-09-483-831B-69	Sequence 69, Appl
719	75.5	2.7	915	5	PCT-US95-06613-69	Sequence 69, Appl
720	75.5	2.7	1207	4	US-09-976-594-4	Sequence 4, Appli
721	75.5	2.7	1646	4	US-09-535-008-67	Sequence 67, Appl
722	75.5	2.7	1647	4	US-09-535-008-2	Sequence 2, Appli
723	75.5	2.7	1647	4	US-09-824-574-4	Sequence 4, Appli
724	75.5	2.7	1647	4	US-09-538-092-1172	Sequence 1172, Ap
725	75.5	2.7	1649	4	US-09-535-008-75	Sequence 75, Appl
726	75.5	2.7	1650	4	US-09-535-008-71	Sequence 71, Appl
727	75.5	2.7	1659	4	US-09-949-016-9752	Sequence 9752, Ap
728	75.5	2.7	1678	4	US-09-535-008-69	Sequence 69, Appl
729	75.5	2.7	1679	4	US-09-535-008-65	Sequence 65, Appl
730	75.5	2.7	1681	4	US-09-535-008-77	Sequence 77, Appl
731	75.5	2.7	1682	4	US-09-535-008-73	Sequence 73, Appl
732	75.5	2.7	2057	4	US-09-499-203-2	Sequence 2, Appli
733	75	2.7	205	4	US-09-248-796A-22069	Sequence 22069, A
734	75	2.7	326	4	US-09-302-626B-54	Sequence 54, Appl
735	75	2.7	357	4	US-09-198-452A-977	Sequence 977, App
736	75	2.7	359	4	US-09-438-185A-906	Sequence 906, App
737	75	2.7	362	4	US-09-248-796A-20514	Sequence 20514, A
738	75	2.7	372	4	US-09-538-092-1035	Sequence 1035, Ap
739	75	2.7	414	4	US-09-583-110-4310	Sequence 4310, Ap
740	75	2.7	415	4	US-09-107-433-3943	Sequence 3943, Ap
741	75	2.7	418	4	US-09-248-796A-18314...	Sequence 18314, A
742	75	2.7	453	3	US-09-134-001C-3749	Sequence 3749, Ap
743	75	2.7	459	4	US-09-248-796A-19036	Sequence 19036, A
744	75	2.7	473	4	US-09-489-039A-9854	Sequence 9854, Ap
745	75	2.7	489	4	US-09-949-016-9590	Sequence 9590, Ap
746	75	2.7	491	4	US-09-710-279-2808	Sequence 2808, Ap
747	75	2.7	522	1	US-08-680-726A-58	Sequence 58, Appl
748	75	2.7	522	3	US-09-092-409-58	Sequence 58, Appl
749	75	2.7	525	3	US-08-984-618-17	Sequence 17, Appl
750	75	2.7	540	3	US-08-964-268-6	Sequence 6, Appli
751	75	2.7	540	4	US-09-105-254-6	Sequence 6, Appli
752	75	2.7	585	4	US-09-489-039A-10279	Sequence 10279, A

753	75	2.7	776	1	US-08-021-601-2	Sequence 2, Appli
754	75	2.7	776	1	US-08-082-849B-2	Sequence 2, Appli
755	75	2.7	776	5	PCT-US94-01624-2	Sequence 2, Appli
756	75	2.7	831	1	US-08-073-384C-5	Sequence 5, Appli
757	75	2.7	831	1	US-08-254-359A-5	Sequence 5, Appli
758	75	2.7	831	1	US-08-483-043-5	Sequence 5, Appli
759	75	2.7	831	1	US-08-481-238-5	Sequence 5, Appli
760	75	2.7	831	2	US-08-471-066B-5	Sequence 5, Appli
761	75	2.7	831	2	US-08-484-956-5	Sequence 5, Appli
762	75	2.7	831	2	US-08-757-653-5	Sequence 5, Appli
763	75	2.7	831	2	US-08-599-491-5	Sequence 5, Appli
764	75	2.7	831	2	US-08-756-386-5	Sequence 5, Appli
765	75	2.7	831	2	US-08-823-516-5	Sequence 5, Appli
766	75	2.7	831	3	US-08-682-853A-5	Sequence 5, Appli
767	75	2.7	831	3	US-08-759-038-5	Sequence 5, Appli
768	75	2.7	831	3	US-08-758-314-5	Sequence 5, Appli
769	75	2.7	831	3	US-09-350-309-5	Sequence 5, Appli
770	75	2.7	831	3	US-08-520-946-5	Sequence 5, Appli
771	75	2.7	831	4	US-09-684-938-5	Sequence 5, Appli
772	75	2.7	831	4	US-09-308-825A-5	Sequence 5, Appli
773	75	2.7	831	4	US-09-758-282B-5	Sequence 5, Appli
774	75	2.7	831	4	US-09-655-378A-5	Sequence 5, Appli
775	75	2.7	831	4	US-09-940-244-5	Sequence 5, Appli
776	75	2.7	831	4	US-09-333-145-5	Sequence 5, Appli
777	75	2.7	831	4	US-09-577-304A-5	Sequence 5, Appli
778	75	2.7	871	4	US-09-792-024-81	Sequence 81, Appl
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780	75	2.7	894	1	US-08-486-924-4	Sequence 4, Appli
781	75	2.7	894	4	US-08-486-929A-4	Sequence 4, Appli
782	75	2.7	990	2	US-08-645-193B-15	Sequence 15, Appl
783	75	2.7	1164	3	US-09-457-708-2	Sequence 2, Appli
784	75	2.7	1164	4	US-09-950-046A-2	Sequence 2, Appli
785	75	2.7	1164	4	US-09-976-594-989	Sequence 989, App
786	75	2.7	1228	4	US-09-949-016-6805	Sequence 6805, Ap
787	75	2.7	1729	4	US-09-134-000C-5675	Sequence 5675, Ap
788	75	2.7	1990	4	US-09-902-540-11251	Sequence 11251, A
789	74.5	2.7	183	4	US-09-270-767-32353	Sequence 32353, A
790	74.5	2.7	183	4	US-09-270-767-47570	Sequence 47570, A
791	74.5	2.7	311	4	US-09-148-545-191	Sequence 191, App
792	74.5	2.7	312	3	US-09-424-349A-5	Sequence 5, Appli
793	74.5	2.7	359	4	US-10-029-180-68	Sequence 68, Appl
794	74.5	2.7	366	4	US-09-501-115-10	Sequence 10, Appl
795	74.5	2.7	380	4	US-09-198-452A-626	Sequence 626, App
796	74.5	2.7	380	4	US-09-438-185A-586	Sequence 586, App
797	74.5	2.7	386	4	US-09-198-452A-1046	Sequence 1046, Ap
798	74.5	2.7	394	4	US-09-438-185A-974	Sequence 974, App
799	74.5	2.7	398	4	US-09-902-540-12305	Sequence 12305, A
800	74.5	2.7	398	6	5187089-7	Patent No. 5187089
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802	74.5	2.7	399	3	US-09-347-801-14	Sequence 14, Appl
803	74.5	2.7	399	4	US-09-854-731-14	Sequence 14, Appl
804	74.5	2.7	409	2	US-08-924-254-2	Sequence 2, Appli
805	74.5	2.7	409	3	US-09-120-249-2	Sequence 2, Appli
806	74.5	2.7	411	3	US-09-347-801-22	Sequence 22, Appl
807	74.5	2.7	411	4	US-09-854-731-22	Sequence 22, Appl
808	74.5	2.7	412	3	US-09-347-801-21	Sequence 21, Appl
809	74.5	2.7	412	4	US-09-854-731-21	Sequence 21, Appl

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811	74.5	2.7	431	3	US-09-111-444-5	Sequence 5, Appli
812	74.5	2.7	431	3	US-09-541-228-5	Sequence 5, Appli
813	74.5	2.7	431	3	US-09-031-295-2	Sequence 2, Appli
814	74.5	2.7	434	4	US-09-543-681A-4577	Sequence 4577, Ap
815	74.5	2.7	440	4	US-10-029-180-124	Sequence 124, App
816	74.5	2.7	451	4	US-10-029-180-123	Sequence 123, App
817	74.5	2.7	458	4	US-09-583-110-5167	Sequence 5167, Ap
818	74.5	2.7	554	1	US-08-106-761-2	Sequence 2, Appli
819	74.5	2.7	554	4	US-08-909-125-7	Sequence 7, Appli
820	74.5	2.7	591	4	US-09-543-681A-5171	Sequence 5171, Ap
821	74.5	2.7	612	4	US-09-248-796A-18848	Sequence 18848, A
822	74.5	2.7	656	4	US-09-489-039A-8212	Sequence 8212, Ap
823	74.5	2.7	720	4	US-09-583-110-2940	Sequence 2940, Ap
824	74.5	2.7	720	4	US-09-107-433-4193	Sequence 4193, Ap
825	74.5	2.7	726	4	US-09-417-197-71	Sequence 71, Appl
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827	74.5	2.7	790	2	US-08-286-846A-9	Sequence 9, Appli
828	74.5	2.7	790	2	US-08-457-880A-9	Sequence 9, Appli
829	74.5	2.7	790	3	US-08-444-622A-9	Sequence 9, Appli
830	74.5	2.7	790	3	US-08-942-562-9	Sequence 9, Appli
831	74.5	2.7	790	3	US-09-156-923-9	Sequence 9, Appli
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833	74.5	2.7	814	2	US-08-441-104A-3	Sequence 3, Appli
834	74.5	2.7	814	2	US-08-440-816A-3	Sequence 3, Appli
835	74.5	2.7	814	3	US-09-417-381A-3	Sequence 3, Appli
836	74.5	2.7	834	3	US-09-143-571-29	Sequence 29, Appl
837	74.5	2.7	834	4	US-09-470-276-2	Sequence 2, Appli
838	74.5	2.7	855	4	US-09-949-016-11016	Sequence 11016, A
839	74.5	2.7	859	4	US-09-538-092-206	Sequence 206, App
840	74.5	2.7	1071	2	US-08-975-527-1	Sequence 1, Appli
841	74.5	2.7	1489	4	US-09-538-092-304	Sequence 304, App
842	74.5	2.7	2262	4	US-09-949-016-8849	Sequence 8849, Ap
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844	74	2.7	397	6	5457090-4	Patent No. 5457090
845	74	2.7	397	6	5187089-9	Patent No. 5187089
846	74	2.7	397	6	5457090-4	Patent No. 5457090
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848	74	2.7	430	4	US-09-198-452A-497	Sequence 497, App
849	74	2.7	430	4	US-09-438-185A-465	Sequence 465, App
850	74	2.7	443	4	US-09-134-000C-4800	Sequence 4800, Ap
851	74	2.7	453	4	US-09-769-863-14	Sequence 14, Appl
852	74	2.7	467	4	US-09-107-532A-6186	Sequence 6186, Ap
853	74	2.7	474	4	US-09-248-796A-15747	Sequence 15747, A
854	74	2.7	481	2	US-08-477-451-19	Sequence 19, Appl
855	74	2.7	501	4	US-09-538-092-692	Sequence 692, App
856	74	2.7	528	4	US-09-710-279-1930	Sequence 1930, Ap
857	74	2.7	557	4	US-09-583-110-4748	Sequence 4748, Ap
858	74	2.7	573	4	US-09-107-433-3736	Sequence 3736, Ap
859	74	2.7	584	4	US-09-604-957-6	Sequence 6, Appli
860	74	2.7	610	4	US-09-248-796A-18471	Sequence 18471, A
861	74	2.7	615	4	US-09-388-743-2	Sequence 2, Appli
862	74	2.7	615	4	US-10-044-543-2	Sequence 2, Appli
863	74	2.7	794	4	US-09-248-796A-20245	Sequence 20245, A
864	74	2.7	830	1	US-07-977-434-6	Sequence 6, Appli
865	74	2.7	830	1	US-08-458-819-6	Sequence 6, Appli
866	74	2.7	830	5	PCT-US91-07035-6	Sequence 6, Appli

867	74	2.7	925	4	US-09-328-352-5244	Sequence 5244, Ap
868	74	2.7	1102	4	US-09-902-540-11735	Sequence 11735, A
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870	74	2.7	1125	4	US-09-949-016-10089	Sequence 10089, A
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872	73.5	2.7	177	4	US-09-543-681A-4212	Sequence 4212, Ap
873	73.5	2.7	185	4	US-09-270-767-41635	Sequence 41635, A
874	73.5	2.7	212	4	US-09-710-279-1128	Sequence 1128, Ap
875	73.5	2.7	239	4	US-09-543-681A-6297	Sequence 6297, Ap
876	73.5	2.7	268	4	US-09-371-338-9	Sequence 9, Appli
877	73.5	2.7	277	4	US-09-803-671B-6	Sequence 6, Appli
878	73.5	2.7	277	4	US-09-803-671B-7	Sequence 7, Appli
879	73.5	2.7	277	4	US-10-274-409-6	Sequence 6, Appli
880	73.5	2.7	277	4	US-10-274-409-7	Sequence 7, Appli
881	73.5	2.7	305	4	US-09-583-110-3421	Sequence 3421, Ap
882	73.5	2.7	313	4	US-09-107-433-4516	Sequence 4516, Ap
883	73.5	2.7	320	3	US-08-793-666-1	Sequence 1, Appli
884	73.5	2.7	392	4	US-09-491-577-76	Sequence 76, Appl
885	73.5	2.7	410	4	US-09-949-016-9327	Sequence 9327, Ap
886	73.5	2.7	422	4	US-09-489-039A-12443	Sequence 12443, A
887	73.5	2.7	441	3	US-09-045-632-37	Sequence 37, Appl
888	73.5	2.7	449	4	US-09-248-796A-14389	Sequence 14389, A
889	73.5	2.7	455	4	US-09-949-016-8345	Sequence 8345, Ap
890	73.5	2.7	508	4	US-09-949-016-8561	Sequence 8561, Ap
891	73.5	2.7	516	2	US-08-676-166A-7	Sequence 7, Appli
892	73.5	2.7	520	4	US-09-949-016-8026	Sequence 8026, Ap
893	73.5	2.7	524	3	US-09-126-420A-24	Sequence 24, Appl
894	73.5	2.7	541	3	US-09-045-632-36	Sequence 36, Appl
895	73.5	2.7	547	4	US-09-134-000C-5974	Sequence 5974, Ap
896	73.5	2.7	566	4	US-09-252-991A-17972	Sequence 17972, A
897	73.5	2.7	596	4	US-09-949-016-9814	Sequence 9814, Ap
898	73.5	2.7	598	4	US-09-134-000C-4957	Sequence 4957, Ap
899	73.5	2.7	599	4	US-09-949-016-6008	Sequence 6008, Ap
900	73.5	2.7	642	3	US-09-045-632-35	Sequence 35, Appl
901	73.5	2.7	659	3	US-09-134-001C-5537	Sequence 5537, Ap
902	73.5	2.7	661	4	US-09-371-338-7	Sequence 7, Appli
903	73.5	2.7	676	4	US-09-134-000C-6050	Sequence 6050, Ap
904	73.5	2.7	740	4	US-09-328-352-8006	Sequence 8006, Ap
905	73.5	2.7	861	3	US-09-045-632-34	Sequence 34, Appl
906	73.5	2.7	871	4	US-09-107-532A-6227	Sequence 6227, Ap
907	73.5	2.7	908	4	US-09-623-326-10	Sequence 10, Appl
908	73.5	2.7	961	3	US-09-045-632-33	Sequence 33, Appl
909	73.5	2.7	997	1	US-08-232-540-1	Sequence 1, Appli
910	73.5	2.7	997	1	US-08-428-949A-1	Sequence 1, Appli
911	73.5	2.7	997	1	US-08-428-948A-1	Sequence 1, Appli
912	73.5	2.7	997	2	US-08-428-946-1	Sequence 1, Appli
913	73.5	2.7	997	5	PCT-US95-04656-1	Sequence 1, Appli
914	73.5	2.7	998	1	US-08-233-008A-6	Sequence 6, Appli
915	73.5	2.7	1005	3	US-09-770-170-4	Sequence 4, Appli
916	73.5	2.7	1021	1	US-08-233-008A-2	Sequence 2, Appli
917	73.5	2.7	1061	3	US-09-045-632-32	Sequence 32, Appl
918	73.5	2.7	1112	3	US-09-045-632-2	Sequence 2, Appli
919	73.5	2.7	1112	3	US-09-045-632-3	Sequence 3, Appli
920	73.5	2.7	1116	4	US-09-583-110-5094	Sequence 5094, Ap
921	73.5	2.7	1120	4	US-09-107-433-3602	Sequence 3602, Ap
922	73.5	2.7	1252	4	US-10-012-762-20	Sequence 20, Appl
923	73.5	2.7	1252	4	US-09-704-036B-20	Sequence 20, Appl

924	73.5	2.7	1403	4	US-09-252-991A-21319	Sequence 21319, A
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926	73.5	2.7	1500	3	US-09-323-472A-12	Sequence 12, Appl
927	73.5	2.7	1500	3	US-09-323-472A-14	Sequence 14, Appl
928	73.5	2.7	1500	4	US-09-585-077C-2	Sequence 2, Appli
929	73.5	2.7	1500	4	US-09-585-077C-12	Sequence 12, Appl
930	73.5	2.7	1500	4	US-09-585-077C-14	Sequence 14, Appl
931	73.5	2.7	1747	4	US-09-949-016-7835	Sequence 7835, Ap
932	73.5	2.7	1927	4	US-09-949-016-6206	Sequence 6206, Ap
933	73.5	2.7	1963	4	US-09-583-110-5243	Sequence 5243, Ap
934	73.5	2.7	1967	4	US-09-107-433-4883	Sequence 4883, Ap
935	73.5	2.7	4536	4	US-09-180-422B-27	Sequence 27, Appl
936	73.5	2.7	4563	4	US-09-108-006C-1	Sequence 1, Appli
937	73.5	2.7	4563	4	US-09-538-092-842	Sequence 842, App
938	73	2.6	200	4	US-09-248-796A-25873	Sequence 25873, A
939	73	2.6	216	4	US-09-710-279-2624	Sequence 2624, Ap
940	73	2.6	268	4	US-09-371-338-13	Sequence 13, Appl
941	73	2.6	274	3	US-09-134-001C-5279	Sequence 5279, Ap
942	73	2.6	291	4	US-09-583-110-5130	Sequence 5130, Ap
943	73	2.6	294	4	US-09-107-433-4874	Sequence 4874, Ap
944	73	2.6	351	1	US-08-324-483-2	Sequence 2, Appli
945	73	2.6	378	3	US-08-158-735A-11	Sequence 11, Appl
946	73	2.6	383	4	US-09-578-063-40	Sequence 40, Appl
947	73	2.6	399	4	US-09-540-236-3640	Sequence 3640, Ap
948	73	2.6	427	4	US-09-489-039A-11442	Sequence 11442, A
949	73	2.6	429	2	US-08-748-485-7	Sequence 7, Appli
950	73	2.6	429	4	US-09-919-039-6	Sequence 6, Appli
951	73	2.6	451	3	US-09-342-647-10	Sequence 10, Appl
952	73	2.6	466	1	US-08-722-001-12	Sequence 12, Appl
953	73	2.6	466	2	US-08-467-568-11	Sequence 11, Appl
954	73	2.6	466	2	US-09-030-582-11	Sequence 11, Appl
955	73	2.6	506	4	US-09-134-000C-6170	Sequence 6170, Ap
956	73	2.6	517	4	US-09-902-540-15269	Sequence 15269, A
957	73	2.6	534	4	US-09-489-039A-8550	Sequence 8550, Ap
958	73	2.6	577	1	US-08-484-105-24	Sequence 24, Appl
959	73	2.6	577	1	US-08-484-106-24	Sequence 24, Appl
960	73	2.6	577	4	US-09-538-092-1306	Sequence 1306, Ap
961	73	2.6	579	1	US-08-126-564A-31	Sequence 31, Appl
962	73	2.6	579	5	PCT-US94-09143-31	Sequence 31, Appl
963	73	2.6	584	4	US-09-107-532A-4564	Sequence 4564, Ap
964	73	2.6	584	4	US-09-949-016-11406	Sequence 11406, A
965	73	2.6	642	4	US-09-371-338-11	Sequence 11, Appl
966	73	2.6	669	2	US-08-357-533A-8	Sequence 8, Appli
967	73	2.6	669	2	US-08-459-009-8	Sequence 8, Appli
968	73	2.6	669	3	US-08-459-951-8	Sequence 8, Appli
969	73	2.6	675	4	US-09-489-039A-9046	Sequence 9046, Ap
970	73	2.6	689	4	US-09-489-039A-7677	Sequence 7677, Ap
971	73	2.6	815	4	US-09-177-165A-24	Sequence 24, Appl
972	73	2.6	854	2	US-08-928-692-17	Sequence 17, Appl
973	73	2.6	854	3	US-09-339-972-17	Sequence 17, Appl
974	73	2.6	1113	3	US-09-629-616-3	Sequence 3, Appli
975	73	2.6	1139	4	US-09-902-540-16085	Sequence 16085, A
976	73	2.6	1182	4	US-09-326-529-4	Sequence 4, Appli
977	73	2.6	1299	3	US-08-460-900C-62	Sequence 62, Appl
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979	73	2.6	1299	3	US-08-954-698-48	Sequence 48, Appl
980	73	2.6	1299	4	US-09-639-695-62	Sequence 62, Appl

981	73	2.6	1299	4	US-09-448-188-48	Sequence 48, Appl
982	73	2.6	1299	4	US-08-954-128-48	Sequence 48, Appl
983	73	2.6	1299	4	US-08-954-740-48	Sequence 48, Appl
984	73	2.6	1319	4	US-09-462-136-4	Sequence 4, Appli
985	73	2.6	1865	1	US-08-588-985-2	Sequence 2, Appli
986	73	2.6	1865	1	US-08-971-988-2	Sequence 2, Appli
987	73	2.6	1865	4	US-09-949-016-6069	Sequence 6069, Ap
988	73	2.6	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
989	73	2.6	2749	4	US-09-385-222A-4	Sequence 4, Appli
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991	73	2.6	3080	6	5223423-4	Patent No. 5223423
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993	72.5	2.6	298	4	US-09-248-796A-19087	Sequence 19087, A
994	72.5	2.6	323	4	US-09-248-796A-15432	Sequence 15432, A
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996	72.5	2.6	346	2	US-08-476-254-10	Sequence 10, Appl
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1002	72.5	2.6	346	6	5474933-7	Patent No. 5474933
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1017	72.5	2.6	603	3	US-09-134-001C-5226	Sequence 5226, Ap
1018	72.5	2.6	603	4	US-09-710-279-1684	Sequence 1684, Ap
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1067	72	2.6	510	4	US-09-742-684A-4	Sequence 4, Appli
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1076	72	2.6	633	4	US-09-824-735-3	Sequence 3, Appli
1077	72	2.6	696	4	US-08-933-711B-7	Sequence 7, Appli
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1084	72	2.6	861	4	US-09-949-016-10418	Sequence 10418, A
1085	72	2.6	997	4	US-09-198-452A-602	Sequence 602, App
1086	72	2.6	1405	4	US-09-438-185A-566	Sequence 566, App
1087	72	2.6	1512	3	US-09-443-184-48	Sequence 48, Appl
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1091	72	2.6	3169	3	US-09-453-702B-257	Sequence 257, App
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1093	71.5	2.6	264	4	US-09-543-681A-6369	Sequence 6369, Ap
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1102	71.5	2.6	405	4	US-09-854-731-20	Sequence 20, Appl
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1104	71.5	2.6	425	4	US-09-902-540-15635	Sequence 15635, A
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1129	71.5	2.6	829	3	US-08-977-221-34	Sequence 34, Appl
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1134	71.5	2.6	836	4	US-09-684-938-162	Sequence 162, App
1135	71.5	2.6	836	4	US-09-684-938-164	Sequence 164, App
1136	71.5	2.6	836	4	US-09-308-825A-162	Sequence 162, App
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1146	71.5	2.6	842	4	US-09-758-282B-157	Sequence 157, App
1147	71.5	2.6	842	4	US-09-577-304A-65	Sequence 65, Appl
1148	71.5	2.6	842	4	US-09-577-304A-157	Sequence 157, App
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1158	71.5	2.6	1138	2	US-08-469-537A-98	Sequence 98, Appl
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1161	71.5	2.6	1285	3	US-08-293-314-2	Sequence 2, Appli
1162	71.5	2.6	2471	3	US-09-112-450-4	Sequence 4, Appli
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1177	71	2.6	340	3	US-09-299-268-32	Sequence 32, Appl
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1183	71	2.6	380	4	US-09-248-796A-20364	Sequence 20364, A
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1188	71	2.6	427	4	US-09-919-497-62	Sequence 62, Appl
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1191	71	2.6	430	3	US-09-541-228-9	Sequence 9, Appli
1192	71	2.6	437	4	US-09-328-352-7401	Sequence 7401, Ap
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1194	71	2.6	467	4	US-09-107-433-3431	Sequence 3431, Ap
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1203	71	2.6	656	4	US-09-949-016-7320	Sequence 7320, Ap
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1207	71	2.6	709	3	US-09-015-003-2	Sequence 2, Appli
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1219	71	2.6	839	4	US-09-577-304A-234	Sequence 234, App
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1230	71	2.6	1440	3	US-09-357-251-37	Sequence 37, Appl
1231	71	2.6	2516	4	US-09-949-016-10280	Sequence 10280, A
1232	71	2.6	3056	1	US-08-508-836A-8	Sequence 8, Appli
1233	71	2.6	3056	2	US-08-629-001A-3	Sequence 3, Appli
1234	71	2.6	3056	2	US-08-874-266-2	Sequence 2, Appli
1235	71	2.6	3056	3	US-08-642-274D-3	Sequence 3, Appli
1236	71	2.6	3056	3	US-08-952-127-3	Sequence 3, Appli
1237	71	2.6	3056	3	US-08-952-014C-3	Sequence 3, Appli
1238	71	2.6	3056	4	US-09-360-416-2	Sequence 2, Appli
1239	71	2.6	3056	4	US-08-984-090-2	Sequence 2, Appli
1240	71	2.6	3057	4	US-09-360-416-3	Sequence 3, Appli
1241	71	2.6	3340	4	US-09-252-991A-23568	Sequence 23568, A
1242	71	2.6	3559	4	US-09-693-205A-10	Sequence 10, Appl
1243	71	2.6	15281	2	US-08-471-119A-2	Sequence 2, Appli
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1245	70.5	2.5	211	4	US-09-451-527-78	Sequence 78, Appl
1246	70.5	2.5	260	4	US-09-322-409-73	Sequence 73, Appl
1247	70.5	2.5	260	4	US-09-451-527-73	Sequence 73, Appl
1248	70.5	2.5	273	4	US-09-328-352-5843	Sequence 5843, Ap
1249	70.5	2.5	273	4	US-08-956-171E-5196	Sequence 5196, Ap
1250	70.5	2.5	273	4	US-09-710-279-752	Sequence 752, App
1251	70.5	2.5	273	4	US-08-781-986A-5196	Sequence 5196, Ap
1252	70.5	2.5	279	4	US-09-328-352-5581	Sequence 5581, Ap
1253	70.5	2.5	291	4	US-09-107-532A-6097	Sequence 6097, Ap
1254	70.5	2.5	296	4	US-09-540-236-2650	Sequence 2650, Ap
1255	70.5	2.5	325	4	US-09-710-279-3296	Sequence 3296, Ap
1256	70.5	2.5	332	4	US-09-561-763-5	Sequence 5, Appli
1257	70.5	2.5	332	4	US-09-431-367B-5	Sequence 5, Appli
1258	70.5	2.5	333	3	US-09-134-001C-5204	Sequence 5204, Ap
1259	70.5	2.5	333	4	US-09-583-110-3052	Sequence 3052, Ap
1260	70.5	2.5	375	4	US-09-107-532A-5089	Sequence 5089, Ap
1261	70.5	2.5	390	3	US-08-460-576-2	Sequence 2, Appli
1262	70.5	2.5	390	4	US-09-134-000C-6192	Sequence 6192, Ap
1263	70.5	2.5	393	4	US-09-270-767-42793	Sequence 42793, A
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1265	70.5	2.5	429	4	US-09-252-991A-22564	Sequence 22564, A

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1270	70.5	2.5	484	4	US-09-710-279-2498	Sequence 2498, Ap
1271	70.5	2.5	485	2	US-08-749-391-2	Sequence 2, Appli
1272	70.5	2.5	485	3	US-09-390-200-2	Sequence 2, Appli
1273	70.5	2.5	509	4	US-09-902-540-12233	Sequence 12233, A
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1276	70.5	2.5	524	3	US-09-542-403-2	Sequence 2, Appli
1277	70.5	2.5	529	1	US-08-548-509-2	Sequence 2, Appli
1278	70.5	2.5	533	4	US-09-328-352-8174	Sequence 8174, Ap
1279	70.5	2.5	538	4	US-09-710-279-260	Sequence 260, App
1280	70.5	2.5	542	4	US-09-107-532A-4858	Sequence 4858, Ap
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1282	70.5	2.5	551	3	US-09-229-059-25	Sequence 25, Appl
1283	70.5	2.5	551	4	US-09-628-133-25	Sequence 25, Appl
1284	70.5	2.5	560	2	US-08-756-317-11	Sequence 11, Appl
1285	70.5	2.5	567	3	US-09-134-001C-5646	Sequence 5646, Ap
1286	70.5	2.5	631	4	US-09-134-000C-6175	Sequence 6175, Ap
1287	70.5	2.5	661	4	US-09-438-185A-803	Sequence 803, App
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1298	70.5	2.5	839	4	US-09-538-092-274	Sequence 274, App
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1307	70.5	2.5	1195	4	US-09-949-016-10747	Sequence 10747, A
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1309	70.5	2.5	1429	4	US-09-358-055B-131	Sequence 131, App
1310	70.5	2.5	1433	4	US-09-543-681A-7342	Sequence 7342, Ap
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1313	70.5	2.5	1500	4	US-09-538-092-1051	Sequence 1051, Ap
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1315	70.5	2.5	2257	4	US-09-839-477-8	Sequence 8, Appli
1316	70	2.5	218	4	US-09-543-681A-7848	Sequence 7848, Ap
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1335	70	2.5	458	4	US-09-673-395A-226	Sequence 226, App
1336	70	2.5	466	1	US-08-334-698-6	Sequence 6, Appli
1337	70	2.5	466	1	US-08-228-932-6	Sequence 6, Appli
1338	70	2.5	466	1	US-08-468-939-6	Sequence 6, Appli
1339	70	2.5	466	1	US-08-722-001-28	Sequence 28, Appl
1340	70	2.5	466	2	US-08-406-855A-6	Sequence 6, Appli
1341	70	2.5	466	2	US-08-722-190-6	Sequence 6, Appli
1342	70	2.5	466	3	US-08-244-354-6	Sequence 6, Appli
1343	70	2.5	466	3	US-09-206-899-6	Sequence 6, Appli
1344	70	2.5	466	4	US-09-444-783-6	Sequence 6, Appli
1345	70	2.5	466	4	US-09-688-415-6	Sequence 6, Appli
1346	70	2.5	466	4	US-09-444-783-6	Sequence 6, Appli
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1350	70	2.5	562	4	US-09-489-039A-8049	Sequence 8049, Ap
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1353	70	2.5	575	4	US-09-543-681A-6584	Sequence 6584, Ap
1354	70	2.5	585	4	US-09-248-796A-17511	Sequence 17511, A
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1357	70	2.5	607	3	US-09-707-802-12	Sequence 12, Appl
1358	70	2.5	607	3	US-09-991-326-12	Sequence 12, Appl
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1366	70	2.5	818	4	US-09-949-016-8579	Sequence 8579, Ap
1367	70	2.5	820	4	US-09-949-016-6134	Sequence 6134, Ap
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1370	70	2.5	846	5	PCT-US95-16435-12	Sequence 12, Appl
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1374	70	2.5	987	2	US-08-436-054-6	Sequence 6, Appli
1375	70	2.5	987	5	PCT-US95-08812-6	Sequence 6, Appli
1376	70	2.5	989	3	US-09-110-517-4	Sequence 4, Appli
1377	70	2.5	989	4	US-09-710-279-2594	Sequence 2594, Ap
1378	70	2.5	990	4	US-09-949-016-7235	Sequence 7235, Ap
1379	70	2.5	998	4	US-09-949-016-8326	Sequence 8326, Ap

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1382	70	2.5	1276	1	US-08-222-616-24	Sequence 24, Appl
1383	70	2.5	1276	3	US-08-446-648-24	Sequence 24, Appl
1384	70	2.5	1276	4	US-09-982-610-24	Sequence 24, Appl
1385	70	2.5	1276	5	PCT-US95-04228-24	Sequence 24, Appl
1386	70	2.5	1967	4	US-09-849-602-16	Sequence 16, Appl
1387	70	2.5	3174	2	US-08-477-451-3	Sequence 3, Appli
1388	69.5	2.5	145	4	US-09-107-532A-6302	Sequence 6302, Ap
1389	69.5	2.5	215	4	US-09-711-164-361	Sequence 361, App
1390	69.5	2.5	220	1	US-07-820-154A-4	Sequence 4, Appli
1391	69.5	2.5	220	2	US-08-097-554A-4	Sequence 4, Appli
1392	69.5	2.5	220	3	US-08-480-640A-4	Sequence 4, Appli
1393	69.5	2.5	220	3	US-08-295-802-4	Sequence 4, Appli
1394	69.5	2.5	220	3	US-08-488-237A-4	Sequence 4, Appli
1395	69.5	2.5	220	3	US-08-375-992A-4	Sequence 4, Appli
1396	69.5	2.5	220	4	US-08-472-679H-4	Sequence 4, Appli
1397	69.5	2.5	220	5	PCT-US93-00324-4	Sequence 4, Appli
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1401	69.5	2.5	230	4	US-09-238-471-18	Sequence 18, Appl
1402	69.5	2.5	262	4	US-09-710-279-876	Sequence 876, App
1403	69.5	2.5	263	3	US-09-134-001C-5231	Sequence 5231, Ap
1404	69.5	2.5	303	4	US-09-543-681A-7924	Sequence 7924, Ap
1405	69.5	2.5	320	3	US-08-793-666-10	Sequence 10, Appl
1406	69.5	2.5	331	4	US-09-107-433-3138	Sequence 3138, Ap
1407	69.5	2.5	337	4	US-09-198-452A-630	Sequence 630, App
1408	69.5	2.5	338	4	US-09-328-352-4723	Sequence 4723, Ap
1409	69.5	2.5	338	4	US-09-248-796A-19784	Sequence 19784, A
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1411	69.5	2.5	344	1	US-08-403-866-9	Sequence 9, Appli
1412	69.5	2.5	345	3	US-09-173-581-6	Sequence 6, Appli
1413	69.5	2.5	345	3	US-09-420-915-6	Sequence 6, Appli
1414	69.5	2.5	355	4	US-09-175-684A-9	Sequence 9, Appli
1415	69.5	2.5	361	4	US-09-175-684A-10	Sequence 10, Appl
1416	69.5	2.5	370	3	US-09-134-001C-3769	Sequence 3769, Ap
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1418	69.5	2.5	379	4	US-09-248-796A-15312	Sequence 15312, A
1419	69.5	2.5	382	3	US-09-134-001C-3447	Sequence 3447, Ap
1420	69.5	2.5	397	4	US-09-438-185A-588	Sequence 588, App
1421	69.5	2.5	398	6	5187089-5	Patent No. 5187089
1422	69.5	2.5	398	6	5187089-5	Patent No. 5187089
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1425	69.5	2.5	477	4	US-09-583-110-3555	Sequence 3555, Ap
1426	69.5	2.5	478	4	US-09-248-796A-20836	Sequence 20836, A
1427	69.5	2.5	479	4	US-09-438-185A-950	Sequence 950, App
1428	69.5	2.5	502	4	US-09-134-000C-4863	Sequence 4863, Ap
1429	69.5	2.5	502	4	US-09-248-796A-14780	Sequence 14780, A
1430	69.5	2.5	503	4	US-09-248-796A-18992	Sequence 18992, A
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1432	69.5	2.5	506	4	US-09-902-540-15114	Sequence 15114, A
1433	69.5	2.5	528	4	US-09-543-681A-4418	Sequence 4418, Ap
1434	69.5	2.5	550	4	US-09-489-039A-13969	Sequence 13969, A
1435	69.5	2.5	560	4	US-09-821-016-3	Sequence 3, Appli
1436	69.5	2.5	560	4	US-10-266-787-3	Sequence 3, Appli

1437	69.5	2.5	613	4	US-09-117-415B-22	Sequence 22, Appl
1438	69.5	2.5	631	4	US-09-117-415B-18	Sequence 18, Appl
1439	69.5	2.5	631	4	US-09-117-415B-20	Sequence 20, Appl
1440	69.5	2.5	633	4	US-09-919-060-13	Sequence 13, Appl
1441	69.5	2.5	649	4	US-09-117-415B-16	Sequence 16, Appl
1442	69.5	2.5	677	3	US-08-480-640A-115	Sequence 115, App
1443	69.5	2.5	677	3	US-08-480-640A-193	Sequence 193, App
1444	69.5	2.5	677	3	US-08-295-802-115	Sequence 115, App
1445	69.5	2.5	677	3	US-08-686-968C-58	Sequence 58, Appl
1446	69.5	2.5	677	3	US-08-686-968C-193	Sequence 193, App
1447	69.5	2.5	677	3	US-08-488-237A-115	Sequence 115, App
1448	69.5	2.5	677	3	US-08-488-237A-193	Sequence 193, App
1449	69.5	2.5	677	3	US-08-375-992A-115	Sequence 115, App
1450	69.5	2.5	677	3	US-08-375-992A-193	Sequence 193, App
1451	69.5	2.5	677	4	US-08-472-679H-115	Sequence 115, App
1452	69.5	2.5	677	4	US-08-472-679H-193	Sequence 193, App
1453	69.5	2.5	721	4	US-08-851-435-2	Sequence 2, Appli
1454	69.5	2.5	746	4	US-08-851-435-6	Sequence 6, Appli
1455	69.5	2.5	789	4	US-09-248-796A-19294	Sequence 19294, A
1456	69.5	2.5	800	4	US-09-270-767-45282	Sequence 45282, A
1457	69.5	2.5	816	4	US-09-248-796A-20939	Sequence 20939, A
1458	69.5	2.5	839	4	US-09-758-282B-230	Sequence 230, App
1459	69.5	2.5	839	4	US-09-577-304A-230	Sequence 230, App
1460	69.5	2.5	864	4	US-09-489-039A-12869	Sequence 12869, A
1461	69.5	2.5	864	4	US-09-751-687-18	Sequence 18, Appl
1462	69.5	2.5	959	4	US-09-248-796A-20776	Sequence 20776, A
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1464	69.5	2.5	1050	4	US-09-902-540-16666	Sequence 16666, A
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1466	69.5	2.5	1087	4	US-09-438-185A-893	Sequence 893, App
1467	69.5	2.5	1091	4	US-10-162-012-15	Sequence 15, Appl
1468	69.5	2.5	1211	4	US-09-328-352-7967	Sequence 7967, Ap
1469	69.5	2.5	1260	3	US-09-245-041-2	Sequence 2, Appli
1470	69.5	2.5	1260	4	US-09-358-055B-2	Sequence 2, Appli
1471	69.5	2.5	1260	4	US-09-893-238-2	Sequence 2, Appli
1472	69.5	2.5	1724	3	US-08-857-076-12	Sequence 12, Appl
1473	69.5	2.5	4866	4	US-09-424-783-2	Sequence 2, Appli
1474	69.5	2.5	6095	3	US-09-144-085-2	Sequence 2, Appli
1475	69	2.5	203	4	US-08-956-171E-5207	Sequence 5207, Ap
1476	69	2.5	203	4	US-08-781-986A-5207	Sequence 5207, Ap
1477	69	2.5	285	4	US-09-328-352-6464	Sequence 6464, Ap
1478	69	2.5	314	4	US-09-583-110-3992	Sequence 3992, Ap
1479	69	2.5	315	4	US-09-107-433-4625	Sequence 4625, Ap
1480	69	2.5	342	4	US-09-248-796A-15902	Sequence 15902, A
1481	69	2.5	358	4	US-09-198-452A-188	Sequence 188, App
1482	69	2.5	358	4	US-09-438-185A-172	Sequence 172, App
1483	69	2.5	369	4	US-09-710-279-1390	Sequence 1390, Ap
1484	69	2.5	369	4	US-09-710-279-1610	Sequence 1610, Ap
1485	69	2.5	372	4	US-09-270-767-46648	Sequence 46648, A
1486	69	2.5	373	4	US-09-248-796A-14832	Sequence 14832, A
1487	69	2.5	385	4	US-09-538-092-333	Sequence 333, App
1488	69	2.5	389	3	US-09-307-621-2	Sequence 2, Appli
1489	69	2.5	393	4	US-09-248-796A-19608	Sequence 19608, A
1490	69	2.5	397	6	5187089-2	Patent No. 5187089
1491	69	2.5	397	6	5187089-2	Patent No. 5187089
1492	69	2.5	407	4	US-09-270-767-43872	Sequence 43872, A
1493	69	2.5	419	2	US-08-933-750C-30	Sequence 30, Appl

1494	69	2.5	419	3	US-09-234-613-30	Sequence 30, Appl
1495	69	2.5	452	4	US-09-248-796A-16171	Sequence 16171, A
1496	69	2.5	455	3	US-09-038-217A-18	Sequence 18, Appl
1497	69	2.5	455	4	US-09-447-034-18	Sequence 18, Appl
1498	69	2.5	467	4	US-09-198-452A-1218	Sequence 1218, Ap
1499	69	2.5	475	3	US-09-212-247C-4	Sequence 4, Appli
1500	69	2.5	484	6	5171673-8	Patent No. 5171673

ALIGNMENTS

RESULT 1

US-09-949-016-5947

; Sequence 5947, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 5947

; LENGTH: 533

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-5947

Query Match 24.5%; Score 679; DB 4; Length 533;

Best Local Similarity 33.8%; Pred. No. 2.4e-63;

Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy	8	LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP	65
		:: :: : ::	
Db	11	LVLGLLLCVLGPVVSAGKILLI-PVDGSHWLSMLGAIQQLQQRGHEIVVL-----AP	62
Qy	66	D---FKKEEKSYQVISWLPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL	111
		: :: : :: :: : : ::	
Db	63	DASLYIRDGAFTLKY--PVPFQREDVKESFVSLGHNVFENDSFLQRFI---KTYKKIK	117
Qy	112	NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFG	171
		:: : ::: :: :	
Db	118	KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC	177
Qy	172	SLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH	228
		: :: : : :	
Db	178	SLEFEATQCPNPFSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE	236

Qy 229 FTEGSRPVLSHLLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIA 288
 | : : || | :| ||| | : ||: || | :||| : | : | : |
 Db 237 FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFGGINCLHQNPLSQEFEAYIN 295
 Qy 289 KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKI 348
 | : | | : :||| : : : : | : || | : | : : : || | :
 Db 296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANTIL 351
 Qy 349 VDWLPQSDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfgdqpenmvrveakkfgv 408
 | ||| : ||| || | | : || | : : | : | : ||| | : ||| | : | | | ||
 Db 352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLEFGDQMDNAKRMETKGAGV 411
 Qy 409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468
 : : : : : | | : | : : || || : | : : | : | | : : : ||
 Db 412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGA 471
 Qy 469 THLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLCGK 505
 || : | | : : : || ||| : | : : |
 Db 472 PHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 508

RESULT 2

US-09-949-016-7684

; Sequence 7684, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7684

; LENGTH: 538

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7684

Query Match 24.5%; Score 679; DB 4; Length 538;

Best Local Similarity 33.8%; Pred. No. 2.4e-63;

Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

Qy 8 LLVGfLL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65

| : : | | | : : | | ||| | | ||| : | | | | | : : | |

Db 16 LVLGLLLcvLGpVvSHAGKILLI-PVDGSHWLSMLGAIQQQLQQRGHEIVVL-----AP 67

Qy 66 D---FKKEEKSYQVISWlapEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111

Db	68	DASLYIRDGAFYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQIRVI---KTYKKIK	122
Qy	112	NVLEYLALQCSHFLNRKDIMDSLKKNENFDMVIVETFDYCPFLIAEKLKPFVAILSTSFG	171
Db	123	KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC	182
Qy	172	SLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH	228
Db	183	SLEFEATQCPNPFYSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE	241
Qy	229	FTEGSRPVLSHLLLKAEWLFINSDFAFDFAFARLLPNTVYVGGLMEKPIKPVQDLENFIA	288
Db	242	FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMVFGGINCLHQNPLSQEFEAYIN	300
Qy	289	KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKI	348
Db	301	ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANNTIL	356
Qy	349	VDWLPQSDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfgdqpenmvrveakkfgv	408
Db	357	VKWLPQNDLLGHPMtraFiThagshgvyesicngvpmvmmpLFGDQMDNAKRMETKGAGV	416
Qy	409	SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA	468
Db	417	TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKA	476
Qy	469	THLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLGCgK	505
Db	477	PHLRPAADLTWYQYHSLDVIGFLLAVVLTVAfITFK	513

RESULT 3

PCT-US92-00282-3

; Sequence 3, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435


```
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 533 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-3
```

```
Query Match          24.3%; Score 674; DB 5; Length 533;
Best Local Similarity 33.8%; Pred. No. 8.2e-63;
Matches 175; Conservative 92; Mismatches 212; Indels 38; Gaps 13;
```

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Qy      8 LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
      |::| || |::| ||| | | ||:| | | | | : |
Db     11 LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQQLQQRGHEIVVL-----AP 62

Qy     66 D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111
      | : :: | : :: | || |::| | ||: | | : : :
Db     63 DASLYIRDGA FYTLKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRVI---KTYKKIK 117

Qy    112 NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFG 171
      | ||| | : |::| || |::: | | | :::| | | |
Db    118 KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC 177

Qy    172 SLEF---GLPIPLSYVPVFRSLTDMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH 228
      |||| | | ||| | : || | ||| | : || | : | :
Db    178 SLEFEATQCPNPF SYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE 236

Qy    229 FTEGSRPVLSHLLLKAE LWFINSDFAFDFARPLL PNTVYVGGLMEKPIKPVQDLENFIA 288
      | : : | | | : | || | : ||::| | :||: | : | : | :
Db    237 FLQ-REVTVQDLLSSASVWLFRSDFVKDYPRPIMPNMV FVGGINCLHQNPLSQEFEAYIN 295

Qy    289 KFGDSGFVLVTLGSMVNTCQNP EIFKEMNNAFAHLPQGV IWKQCQSHWPKDVH LAANVKI 348
      | : | | : ||||: | : : | | | : | : : : | : | :
Db    296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKNPQTVLWRYTGT---RPSNLANNTIL 351

Qy    349 VDWL PQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVG IPLFGDQPENMVRVEAKKFGV 408
      | |||: || | | |::| | : : | : |::| | :||| | : | | |
Db    352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMP LFGDQMDNAKRMETKGAGV 411

Qy    409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468
      : : : : : | | : | : || || | : : | : | | : : | : |
Db    412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGA 471

Qy    469 THLKPYVFQQPWHEQYLFDFV FVLLGLTLGLTLWL CGK 505
      ||:| | : : || ||| : | : : |
Db    472 PHLRPA AHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 508
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RESULT 4

US-09-949-016-8465

; Sequence 8465, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8465

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-8465

Query Match 24.0%; Score 663.5; DB 4; Length 540;

Best Local Similarity 34.2%; Pred. No. 1.1e-61;

Matches 173; Conservative 88; Mismatches 214; Indels 31; Gaps 15;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
 ||:: : : | || ||:| | | | | :: || ::
 Db 46 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLTKTEFEDIKQL 105
 Qy 90 KKSFDFFLEETLGGRGKFENLLNVL----EYLALQCSHFLNRKDIMDSLKNENFDMVIVE 145
 | : ::| | : :: : | | :: | :| | : ||:: :
 Db 106 VKRWAELPKDFTW--SYFSQVQEIMWTFNDILRKFCCKDIVSNKKLMKKLQESRFDVVLAD 163
 Qy 146 TFDYCPF--LIAEKLGPFFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWG 199
 || |::| | || | | | ::| || | |||| | |::| | |
 Db 164 A--VFPPGELLAELLKIPFVYSLRFSPGYAIEKHSGGLFPFSPYVPMSELSDQMTFIE 221
 Qy 200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
 |||| ::::| | : | : | | | | | : ||::| | : : | |
 Db 222 RVKNMIYVLYFEFWQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 278
 Qy 258 ARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
 |||| |::| | || ||:::| | : |::| | : :||| | | : | :
 Db 279 PHLLPNVEFVGGLHCKPAKPLPKEMEETFQSSGENGVVVSLSGSMVSNSTSE--ERANVI 336
 Qy 317 NNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLFTVTHGGQNSIM 376
 : | | :|| |:: : | | | :: |::||| | | | :||| | |
 Db 337 ASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 393
 Qy 377 EAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
 ||| ||::|||:||| ||::| :::| || : : | :| :: | ||

Db 394 EAIYHGIPMVGVPFLFADQPDNIAHMKAKGAAVSLDFHTMSSTDLLNALKTVINDPLYKEN 453

Qy 437 AVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDDVVFLLGLT 496
 |: | | |: | :| | |: |: | | | | : : | | | |

Db 454 AMKLSRIHHDQPVKPLERAVFWIEFVMRHKGAKHLRVAHDLTWFQYHSLDVTGFLACV 513

Qy 497 LGTLWLCCGKLLGMAVW-WLRGARKVK 521
 :: | | | | :| :| |

Db 514 ATVIFIITKCL-FCVWKFVRTGKKGK 538

RESULT 5

US-09-949-016-9052

; Sequence 9052, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 9052

; LENGTH: 540

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-9052

Query Match 24.0%; Score 663.5; DB 4; Length 540;

Best Local Similarity 34.2%; Pred. No. 1.1e-61;

Matches 173; Conservative 88; Mismatches 214; Indels 31; Gaps 15;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSYQVISWLAPEDHQREF 89

||:: : : | || ||:| | | | : | | :

Db 46 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLTKTEFEDIKQL 105

Qy 90 KKSFDFFLEETLGGRGKFENLLNVL----EYLAQCASHFLNRKDIMDSLKNENFDMVIVE 145.....

| : : : | : : : | : : | : | : | : | : | :

Db 106 VKRWAELPKDTFW--SYFSQVQEIMWTFNDILRKFKCDIVSNKKLMKKLQESRFDVVLAD 163

Qy 146 TFDYCPF--LIAEKLGPFFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLTDMDFWG 199

|| |:| | || | | | :| | | | | | | | | | |

Db 164 A--VFPFGELLAELLKIPFVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSQMTFIE 221

Qy 200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWLWFINSDFAFDF 257

|||| ::::| | : | : | | | | : | | : | | : | |

Db 222 RVKNMIYVLYFEFWFQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 278

Qy	258	ARPLLNTVYVVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM	316
Db	279	PHPLLENVVEFVGGLHCKPAKPLPKEMEEFVQSSGENGVVVSFLGSMVSNTSE--ERANVI	336
Qy	317	NNAFAHLPGQVIWKQCQSHWP KDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIM	376
Db	337	ASALAKIPQKVLWRF DGN---KPD TLGLNTRLYKWIPQNDLLGH PKTRAFITHGGANGIY	393
Qy	377	EAIQHGVPMVGIP LFGDQ PENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA	436
Db	394	EAIYHGIPMGVPLFADQPDNIAHMKAKGA AVSLDFHTMSSTDLLNALKTVINDPLYKEN	453
Qy	437	AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKP YVFQQPWHEQYLFDFVFLLGLT	496
Db	454	AMKLSRIHHDQPVKPLERAVFEWIEFVMRHKGAKHLRVA AHDLTW FQYHSLDVTGFLLACV	513
Qy	497	LGTLWL CGKLLGMAVW-WLRGARKVK	521
Db	514	ATVIFIITKCL-FCVWK FVRTGKKGK	538

Query Match 23.9%; Score 661.5; DB 4; Length 528;
Best Local Similarity 34.2%; Pred. No. 1.7e-61;
Matches 173; Conservative 87; Mismatches 215; Indels 31; Gaps 15;

Qy 146 TFDYCPF--LIAEKLGPVFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLTLDHMDFWG 199
 || |::| | || | | |::| || | |||| | |::| |
 Db 152 A--VFPFGELLAELLKIPFVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209
 Qy 200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
 |||| ::::| | : | : | | | | : ||::| | : : | |
 Db 210 RVKNMIYVLYFEFWFQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266
 Qy 258 ARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
 |||| :||| || ||:::| | : |::| | : : |||| | | : | :
 Db 267 PHLLPNVEFVGGLHCCKPAKPLPKEMEEFVQSSGENGVVVSLSGSMVSNSTSE--ERANVI 324
 Qy 317 NNAFAHLPPQGVWKQCQSHWPKDVHLAANVKIWDWLPQSDLLAHPSIRLFVTHGGQNSIM 376
 :| | :|| |:: : | | | : : |::||| || | |::||| | |
 Db 325 ASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWI PQNDLLGHPKTRAFITHGGANGIY 381
 Qy 377 EAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
 ||| ||::|||:||| ||::: :::| ||: : : | :| : : | ||
 Db 382 EAIYHGIPMVGVPPLFADQPDNIAHMKAKGAASLDFTMSSTDLLNALKTVINDPLYKEN 441
 Qy 437 AVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLT 496
 |: | | | : | | ||: |:: || ||: | : : || |||
 Db 442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHDLTWFAQYHSLDVTGFLACV 501
 Qy 497 LGTLWLCGKLLGMAVW-WLRGARKVK 521
 :: : | | || : : | : |
 Db 502 ATVIFIITKCL-FCVWKFVRTGKKGK 526

RESULT 7

PCT-US92-00282-6

; Sequence 6, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

```

; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-6

```

```

Query Match          23.8%; Score 658; DB 5; Length 531;
Best Local Similarity 30.9%; Pred. No. 4.2e-61;
Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

```

```

Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
      : |   |||:   ||   :|   |:| : : |||:| |   | : |   ||   :|
Db      7 LRGLSGLLLLLCALP---WAEGGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAP---EDHQREF----KKSFD-----FFLEETLGGRGK 106
      | :   | | : : :: |   |:|||   || | :   ||   ||:   |
Db     59 APEVTVHMKGEDFFTLQTYAFPYTKEEYQREILGNAKKGFEPQHFVKTFE--ETMASIKK 116

Qy    107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAIL 166
      | :|   |   | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db    117 FFDL-----YANSCAALLHNKTLIQQLNSSSFDVVLTDPVFPCGALLAKYLQIPAVFFL 170

Qy    167 STSFGSLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFS---FCRRQQHMQST 220
      :   : ::   | | |||:|   :|:| || |   ||| |   :   |   | : |
Db    171 RSVPCGIDYEATQCPKPSSYIPNLLTMSLDHMTFLQRVKNMLYPLTLKYIC----HLSIT 226

Qy    221 FDNTIKEHFTEGSR---PVLSHLLLLKAELWFINSDFAFDFARPLLNPNTVYVGGLMEKPIK 277
      : :   :   ||||   | :|   || ||: ||: ||| | :| :| :|
Db    227 PYESLASELLQREMSLVEVLSH----ASVWLFVRGDFVFDYPRPIMPNMVFIGGINCVIKK 282

Qy    278 PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShWP 337
      | :| :| : :| :| | :| :| ||||:   :   | :| |   :| :| :| :|
Db    283 PLSQFEAYVNASGEHGIVVFSLGSVMSEIPEKKAM-EIAEALGRIPQTLWRYTGT--- 338

Qy    338 KDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPEN 397
      : :|| |   :| ||||: ||| || | | :|| | :| | | :||| | :||| | :|
Db    339 RPSNLAKNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLFQDQMDN 398

Qy    398 MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG 457
      |:| :   ||: : : :| :|   :| : : :| ||   :   | : :   | :| |
Db    399 AKRMETRGAGVTNLVLEMTADDLENALKTVINNKSYPKENIMRLSSLHKDRPIEPLDLAVF 458

Qy    458 WIDHVLQTTGGATHLKPYPVFQPPWHEQYLFDFVFVLLGLTLGLTLWL-----CGKLLGM 509
      | : :| : :| || ||:|   |: :   ||   ||| :|   : :   | | |
Db    459 WVEYVMRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG- 517

Qy    510 AVWWLRGARKVKET 523
      |   :| : :
Db    518 -----GKGRVKKS 525

```

RESULT 8

US-09-180-852-2

; Sequence 2, Application US/09180852

; Patent No. 6287834

; GENERAL INFORMATION:

; APPLICANT: BELANGER, Alain

; APPLICANT: HUM, Dean W.

; APPLICANT: BEAULIEU, Martin

; APPLICANT: LEVESQUE, Eric

; TITLE OF INVENTION: CHARACTERIZATION AND USE OF AN ISOLATED URIDINE

; TITLE OF INVENTION: DIPHOSPHO-GLUCURONOSYLTRANSFERASE

; FILE REFERENCE: 1259-449

; CURRENT APPLICATION NUMBER: US/09/180,852

; CURRENT FILING DATE: 1999-02-08

; EARLIER APPLICATION NUMBER: PCT/CA97/00328

; EARLIER FILING DATE: 1997-05-16

; EARLIER APPLICATION NUMBER: US 08/649,319

; EARLIER FILING DATE: 1996-05-17

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 530

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-180-852-2

Query Match 23.7%; Score 657; DB 3; Length 530;

Best Local Similarity 32.6%; Pred. No. 5.3e-61;

Matches 159; Conservative 92; Mismatches 211; Indels 26; Gaps 11;

```

Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSQVI-SWLAPEDHQREFKKS 92
      ||:: | : : | || | : | : | : | : | : | : |
Db      34 SHWINMKTILEELVQRGHEVIVLTSSASILVNASKSSAIKLEVYPTSLTKNDLEDFFMKM 93

Qy      93 FDFLEETLGGRGKFENLLNVLEYLALQCSHF-----LNRKDIMDSLKNENFDMVI 143
      || : : | : : | : | : | : | : | : | : | : | : |
Db      94 FDRWTYSI--SKNTFWSYFSQLQELCWEYSYDYNIKLCEDAVLNKK-LMRKLQESKFDVLL 150

Qy     144 VETFDYCPFLIAEKLGPVFAILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWG 199
      : : | | : | | || : | | | : | | | | | | | | | |
Db     151 ADAVNPCGELLAELLNIPFLYSLRFSVGYTVEKNGGGFLFPPSYVPVVMSELSQMI FME 210

Qy     200 RVKN--FLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDF 257
      | : | : : : | | : : : | | | | | | : | | : | : |
Db     211 RIKNMIYMLYFDFWFQAYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEF 267

Qy     258 ARPLLNPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP EIFKEMN 317
      || || | : || | || | : : | | : : | : : | : : | : |
Db     268 PRPFLPNVDFVGGHLHCKPAKPLPKEME EFVQSSGENGIVVFSLGSMISN-MSEESANMIA 326

Qy     318 NAFALPQGVIVKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIME 377
      : | | : | | | : | | : | : | | | : | | : | | | | |
Db     327 SALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLPQNDLLGHPKTKAFITHGGTNGIYE 383

Qy     378 AIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAA 437

```

```

      || ||:|||||| || :|:  ::||  :|: :: : : |  :| :: | ||
Db      384 AIYHGIPMVGIPLFADQHDNIAHMKAKGAALSVDIRTMSSRDLLNALKSVINDPIYKENI 443
Qy      438 VAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQYLFDFVFLGLTL 497
      : | |  | : | | | ||: ||: || ||:  | : : || |||
Db      444 MKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIQYHSLDVIAFLLACVA 503
Qy      498 GTLWLCCGK 505
      ::: |
Db      504 TMIFMITK 511

```

RESULT 9

US-09-356-806-40

; Sequence 40, Application US/09356806

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

; TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 40

; LENGTH: 524

; TYPE: PRT

; ORGANISM: H. sapiens

US-09-356-806-40

Query Match 23.5%; Score 651.5; DB 4; Length 524;

Best Local Similarity 31.5%; Pred. No. 2e-60;

Matches 163; Conservative 87; Mismatches 212; Indels 55; Gaps 14;

```

Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-PFMPD-----FKKEEKSY---Q 75
      ||:: : : | || ||:|  | |:  | |:: |
Db      34 SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSALKIEIYPTSLTKTELENFIMQQ 93
Qy      76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDS 133
      : |  |:|  : : : : : : : |  :: | |
Db      94 IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCCKDVVSNKKFMKK 139
Qy      134 LKNENFDMVIVETFDYCPFLIAEKLGPVFVAILSTS----FGSLEFGLPIPLSYVPVFRS 189
      :: ||:: : | |:|  ||| || |  |  | |||| |
Db      140 VQESRFDVIFADAIFFPCSELLAELFNIPFVYSLSFSPGYTFEKHSGGFIFPPSYVPVVMMS 199
Qy      190 LLTDHMDFWGRVKN--FLMFFSFCCRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLLLKA 244
      ||| | | |||| ::::| |  ||  : |  |  || : ||
Db      200 ELTDQMTFMERVKNMIYVLYFDF-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA 253
Qy      245 ELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMV 304

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      ::| | : : | | |||| :||| || ||:|::|:|: |::| | : ||||
Db      254 DVWLIRNSWNFQFPYPLLPNVDFVGGHLCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV. 313

Qy      305 NTCQNPEIFKEMNNAFAHLPQGVIWKCQCQSHWPKDVHLLAANVKIVDWLPQSDLLAHPSIR 364
      : | : :| | :|| |:: : | | | : : |::||| || |
Db      314 SN-MTEERANVIASALAQIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTR 369

Qy      365 LFTVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
      |::||| | | ||| ||:||||||| ||::|: ::|: | : : : | :
Db      370 AFITHGGANGIYEAIYHGIPMVGIPLFADQPDNIAHMKARGAAVRVDFNTMSSTDLLNAL 429

Qy      425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484
      |::: | || : | | | : | | ||: |:: || ||: | : :
Db      430 KRVINDPSYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAAHDLTWFAQYH 489

Qy      485 LFDVFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVK 521
      || ||| ::: | | : ||| |
Db      490 SLDVIGFLLVCVATVIFIVTKCCLFCFW--KFARKAK 524

```

RESULT 10

US-09-949-016-8605

; Sequence 8605, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 8605

; LENGTH: 439

; TYPE: PRT

; ORGANISM: Human

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: (1)...(439)

; OTHER INFORMATION: Xaa = Any Amino Acid

US-09-949-016-8605

Query Match 23.4%; Score 649; DB 4; Length 439;

Best Local Similarity 34.4%; Pred. No. 2.8e-60;

Matches 147; Conservative 74; Mismatches 184; Indels 22; Gaps 8;

```

Qy      106 KFENLLNVLEYLALQ-CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFVA 164
      |: :::: : : | :: | | :: ||:: : | |::| ||
Db      21 KYREIMSIFGDITRKFCCKDVVSNKKFMKKVQESRFDVIFADAI FPCSELLAE LFNIPFVY 80

```

Qy	165	ILSTS---FGSLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKN--FLMFFSFCRRQQHMQ	218
Db	81	SLSFSPGYTFEKHSGGFIFFPSYVPVVMSELTDQMTFMERVKNMIYVLYFDF-----WF	134
Qy	219	STFDNTIKEHFTE---GSRPVLSHLLLKAEWLFINSDFAFDFARPLLNTVYVGGLMEKP	275
Db	135	EIFDMKKWDQFYSEVLGRPTTLSETMGKADVWLIRNSWNFQFPYPLLPNVDFVGGHLCKP	194
Qy	276	IKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSH	335
Db	195	AKPLPKEMEDFVQSSGENGVVFSLSGSMVSN-MTEERANVIASALAQIPQKVLWRFDGN-	252
Qy	336	WPKDVHLAANVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFQDQP	395
Db	253	--KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFADQP	310
Qy	396	ENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRL	455
Db	311	DNIAHMKARGAAVRVDFNTMSSTDLLNALKRVIDNPSYKENVMKLSRIQHDQPVKPLDRA	370
Qy	456	VGWIDHVLQTTGATHLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLCCGKLLGMAVWWLR	515
Db	371	VFWIEFVMRHKGAKHLRVAAHDLTWFOYHSLDVIGFLLVCVATVIFIVTKCCLFCFW--K	428
Qy	516	GARKVKE	522
Db	429	FARKAKK	435

US-09-356-806-113

; Patent No. 6586175

; GENERAL INFORMATION:

; APPLICANT: Penny, Laura

; APPLICANT: Galvin, Margaret

; APPLICANT: Miller, Andrew

; APPLICANT: Reidy, Michael

; TITLE OF INVENTION: Genotyping Human

: TITLE OF INVENTION: UDP-Glucuronosyltransferase 2B4 (UGT2B4), 2B7 (UGT2B7)

and

; TITLE OF INVENTION: 2B15 (UGT2B15) Genes

; FILE REFERENCE: SEQ-22PRV2

; CURRENT APPLICATION NUMBER: US/09/356,806

; CURRENT FILING DATE: 1999-07-20

; NUMBER OF SEQ ID NOS: 164

```
; SOFTWARE: FastSEO for Windows Version 3.0
```

; SEO ID NO 113

; LENGTH: 530

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; TYPE: PRT
```

; ORGANISM: H. sapiens

US-09-356-806-113

Query Match 23.4%; Score 649; DB 4; Length 530;

Best Local Similarity 31.8%; Pred. No. 3.8e-60;

Matches 155; Conservative 90; Mismatches 218; Indels 24; Gaps 10;

Qy	34	SHYLLMDRVSQILQDHHGNVTMLNHKRGPFMPDFKKEEKSYQVI-SWLAPEDHQREFKKS	92
Db	34	SHWINMKTILEELVQRGHEVTVLTSSASTLVNASKSSAIKLEVYPTSLTKNDLEDSSLKI	93
Qy	93	FDFFLLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV	144
Db	94	LDRWIYGV--SKNTFWSYFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILA	151
Qy	145	ETFDYCPFLIAEKLGPVFAVILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWGR	200
Db	152	DALNPCGELLAELEFNIPFLYSLRFSVGYTFEKNNGGGFLFPPSYVPVVMSELSDQMIFMER	211
Qy	201	VKNF--LMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDFA	258
Db	212	IKNMIHMLYDFDFWFIQYDLKK-WDQFYSE--VLGRPTTLFETMGKAEMWLIRTYWDFEFP	268
Qy	259	RPLLNPNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN	318
Db	269	RPFLPNVDFVGGHLCKPAKPLPKEMEETFVQSSGENGIVVFSLGSNISN-MSEESANMIAS	327
Qy	319	AFAHLPPQGVIIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEA	378
Db	328	ALAQIPQKVLWRFD---GKKPNTLGSNTRLYKWLQNDLLGHPKTKAFITHGGTNGIYEA	384
Qy	379	IQHGVPVMVGIIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAV	438
Db	385	IYHGIPMVGIIPLFADQHDNIAHMKAKGAALSVDIRTMSRDLNALKSVINDPVYKENVM	444
Qy	439	AASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFOQPWHEQYLFDFVFLLGLTLG	498
Db	445	KLSRIHHDQPMKPLDRAVFWIEFVMRHKGAKHLRVAAHNLTWIIQYHSLDVIAFLLACVAT	504
Qy	499	TLWLCGK	505
Db	505	VIFIITK	511

US-09-949-016-6999

; GENERAL INFORMATION:

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6999
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6999.

Query Match 22.9%; Score 632.5; DB 4; Length 528;
Best Local Similarity 33.4%; Pred. No. 2.2e-58;
Matches 169; Conservative 88; Mismatches 218; Indels 31; Gaps 15;

Qy 34 SHYLLMDRVSQILQDHGHNVTMLNHKRG-----PFMPDFKKEEKSYQVISWLAPEDHQREF 89
| | : : : | | | | : : | | : :
Db 34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLTKTEFEDIKQL 93

Qy 90 KKSFDFFLEETLGGRGKFENLLNVL----EYLALQCSHFLNRKDIMDSLKNENFDMVIVE 145
| : : : | : : : | : : | : | : | : | :
Db 94 VKRWAELPKDTFW--SYFSQVQEIMWTFNDILRKFKCKDIVSNKKLMKKLQESRFDVVLAD 151

Qy 146 TFDYCPF--LIAEKLKGPFAVAILSTSFG-SLE---FGLPIPLSYVPVFRSLLTDHMDFWG 199
| | | : | | | | : : | | | | | | : | | |
Db 152 A--VFPFGELLAELLKIPFVYRPRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQMTFIE 209

Qy 200 RVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLLKAELWFINSDFAFDF 257
| | | : : : | : : : | : : | : | : | : : |
Db 210 RVKNMIYVLYFEFWQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYWDFQF 266

Qy 258 ARPLLNPNTVYVGGLMKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEIFKEM 316
| | | : | | | | | : : : | : : | : | : | : :
Db 267 PHPLLNPVEFVGGLHCKPAKPLPKEMEETFVQSSGENGVVFSLGSMVSNTSE--ERANVI 324

Qy 317 NNAFAHLPPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIM 376
: | : | : : : : | : : : : : | : : | : | : | : |
Db 325 ASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGANGIY 381

Qy 377 EAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSA 436
: | : : | : | : : : : : : : : : : : : : : | : : : | : |
Db 382 KAISPRIPMVGVPFLFADQPDNIAHMKAKGAAVSLDFHTMSSTDLLNALKTVINDPLYKEN 441

Qy 437 AVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYVFQQPWHEQYLFDFVFLGLT 496
| : | | : : | | | : : : | | : : : : | : : | | |
Db 442 AMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHADLTWFQYHSLDVTGFLACV 501

Qy 497 LGTLWLCGKLLGMAVW-WLRGARKVK 521
: : : | | | : : : | : |
Db 502. ATVIFIITKCL-FCVWKFFVRTGKKGK 526

RESULT 13

PCT-US92-00282-5

; Sequence 5, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/00282
; FILING DATE: 19920110
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SCOTT, WATSON T.
; REGISTRATION NUMBER: 26581
; REFERENCE/DOCKET NUMBER: 91532-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-00282-5

```

```

Query Match          22.7%; Score 629; DB 5; Length 531;
Best Local Similarity 30.4%; Pred. No. 5.3e-58;
Matches 159; Conservative 100; Mismatches 218; Indels 46; Gaps 13;

```

```

Qy      4 QRVLLLVGFL-LPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      ||:  | || | |:::  : |::  :  ||::| |  : ::| | | : ::
Db      9 QRISAGVFFLALWGMVVGDD--KLLVVPQ-DGSHWLSMKDIVEVLSDRGHEIVVV----- 59

Qy     63 FMPDFK---KEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRG-----KFENLLN 112
      :|:  || | |  : | | | | | : |  |  : : | :
Db     60 -VPEVNLLLKEYKYYTRKIYPVPYD-QEELKNRYQSFGNNHFAERSFLTAPQTEYRNNMI 117

Qy    113 VLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGS 172
      |:  : |  | :| :: |  || :  :  | :|| || | | :  |
Db    118 VIGLYFINCQSLLQDRDTLNFFKESKFDALFTDPALPCGVILAEYLGLPSVYLFRGFPCS 177

Qy    173 LEFGL---PIPLSYVPVFRSLLTDHMDFWGRVKNFL-----MFFSFCRRQQHMQSTFD 222
      ||  | |::| |  : :|| | | || ||  :|:  : : : |
Db    178 LEHTFSRSPDPVSYIPRCYTKFSDHMTFSQRVANFLVNLLEPYLFYCLFSKYEKLASA-- 235

Qy    223 NTIKEHFTEGSRPVLSHLLKAEWLFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQD 282
      :|  | |  | : :| : || :|::|| |::||: | | : |:
Db    236 -VLK-----RDVDIITLSEVSVWLLRYDFVLEYPRPVMNMFVFIGGINCKKRKDLSEQ 287

```

Qy 283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHL 342
 | : | | : | | : : | | | : : : : |
 Db 288 FEAYINASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKNPQTVLWRYTGT---RPSNL 343

Qy 343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVE 402
 | | : | | | : | | | | : | | : : | : | : | | | : | | : |
 Db 344 ANNTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPLFGDQMDNAKRME 403

Qy 403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
 | | : : : : | | : | : | | | : | : : | : | | : : |
 Db 404 TKGAGVTLNPLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFV 463

Qy 463 LQTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLTLGLTLWLCGK 505
 : : | | | : | | : : | | | : | : : |
 Db 464 MRHKGAPHLRPAAHDLTWYQYHSLDVIGFLLAVVLTVAFITEK 506

RESULT 14

PCT-US92-00282-4

; Sequence 4, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/00282

; FILING DATE: 19920110

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: SCOTT, WATSON T.

; REGISTRATION NUMBER: 26581

; REFERENCE/DOCKET NUMBER: 91532-PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-861-3000

; TELEFAX: 202-822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 534 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US92-00282-4

Query Match 21.9%; Score 606; DB 5; Length 534;
Best Local Similarity 31.3%; Pred. No. 1.5e-55;
Matches 163; Conservative 94; Mismatches 218; Indels 46; Gaps 13;

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Qy      8 LLVGFLLPGVLLS-----EAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     12 LATGLLL---LLSVQPWAESGKVLVPT-DGSPWLSMREALRELHARGHQAVVLT----P 63

Qy     63 FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLG---GRGKFENLL----- 111
      : | | | | : : : | | : | : | | | | | | | | | | | |
Db     64 EVNMHIKEEKFFTLTAYAVPWT-QKEFDR-----VTLGYTQGGFFETEHLKRYSRMA 115

Qy    112 ---NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILST 168
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    116 IMNNVSLALHRCCVELLHNEALIRHLNATSFDDVLTDPVNLGAVLAKYLSIPAVFFWRY 175

Qy    169 SFGSLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTI 225
      | : | | | | | | | | | | | | | | | | | | | | | |
Db    176 IPCDLDFKGTQCPNPSSYIPKLLTNSDHMTFLQRVKNMLYPLALSICHTFSAFYASLA 235

Qy    226 KEHFTEGSRPV-LSHLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLE 284
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    236 SELF---QREVSVDLVSYASVWLFGRDFVMDYPRPIMPNMVFIGGINCANGKPLSQEFE 292

Qy    285 NFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCQSHWPKDVLHAA 344
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db    293 AYINASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLAN 348

Qy    345 NVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAK 404
      | : | | | | | | | | | | | | | | | | | | | | | | | |
Db    349 NTILVKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPPLFGDQMDNAKRMETK 408

Qy    405 KFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQ 464
      | | : : : : | | | | | | | | | | | | | | | | | |
Db    409 GAGVTLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMR 468

Qy    465 TGGATHLKPYVFQQPWHEQYLFDFVFLGLGLTLGLTLWLCGK 505
      | | | | | | | | | | | | | | | | | | | | | |
Db    469 HKGAPHLRPAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 509
```

RESULT 15

PCT-US92-00282-7

; Sequence 7, Application PC/TUS9200282

; GENERAL INFORMATION:

; APPLICANT: OWENS, IDA S.

; APPLICANT: RITTER, JOSEPH K.

; TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION

; TITLE OF INVENTION: THEREIN.

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN DARBY & CUSHMAN

; STREET: 1615 L STREET, N.W.

; CITY: WASHINGTON

; STATE: D.C.

Db	343	KNTILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMMPLEFGDQMDNAKRMET	402
Qy	404	KKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVL	463
Db	403	RGAGVTNLNVLEMTADDLENALKTVINNKSYPENIMRLSSLHKDRPIEPLDLAVFWVEYVM	462
Qy	464	QTGGATHLKPYPVFQQPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLGMAVWWLR	515
Db	463	RHKGAPHLRPAADLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG-----	515
Qy	516	GARKVKET	523
Db	516	GKGRVKKS	523

Search completed: February 15, 2005, 12:54:31
Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 15, 2005, 12:26:43 ; Search time 40 Seconds
(without alignments)
1258.034 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWVWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	700	25.3	541	2	JC5423	2-hydroxyacylsphin
2	684	24.7	541	2	A48801	2-hydroxyacylsphin
3	679	24.5	533	2	A39092	glucuronosyltransf
4	674.5	24.4	530	2	A40467	glucuronosyltransf
5	671	24.2	529	2	A42233	glucuronosyltransf
6	670	24.2	531	2	B47113	glucuronosyltransf
7	662.5	23.9	530	2	C47113	glucuronosyltransf
8	658	23.8	531	2	A35343	glucuronosyltransf
9	658	23.8	535	2	I57961	glucuronosyltransf
10	656.5	23.7	528	2	JN0619	glucuronosyltransf
11	654.5	23.6	529	2	A35366	glucuronosyltransf
12	650	23.5	527	2	S15089	glucuronosyltransf
13	649	23.4	530	2	A48633	glucuronosyltransf

14	642	23.2	528	2	JN0620	UDP-glucuronosyltr
15	640	23.1	530	2	S07390	glucuronosyltransf
16	639	23.1	530	2	A36276	glucuronosyltransf
17	637.5	23.0	530	2	S00163	glucuronosyltransf
18	632.5	22.9	530	2	S68200	glucuronosyltransf
19	632	22.8	523	2	S11309	glucuronosyltransf
20	629	22.7	531	2	A31340	glucuronosyltransf
21	623	22.5	530	2	JC5656	UDP glucuronosyltr
22	622.5	22.5	529	2	JE0200	orphan UDP-glucuro
23	612.5	22.1	531	2	A55788	glucuronosyltransf
24	610	22.0	530	2	S17512	glucuronosyltransf
25	600	21.7	529	2	A24600	glucuronosyltransf
26	596.5	21.5	531	2	B55788	glucuronosyltransf
27	513	18.5	485	2	T13694	glucuronosyltransf
28	471	17.0	949	2	T18591	hypothetical prote
29	455.5	16.5	534	2	T34455	hypothetical prote
30	449	16.2	531	2	T33980	hypothetical prote
31	448	16.2	573	2	T27578	hypothetical prote
32	447	16.1	531	2	T23835	hypothetical prote
33	441.5	16.0	508	2	T03910	UDP-glucuronosyltr
34	438	15.8	534	2	T19944	hypothetical prote
35	427	15.4	586	2	T19075	hypothetical prote
36	424	15.3	534	2	T19951	hypothetical prote
37	419	15.1	533	2	T34458	hypothetical prote
38	412.5	14.9	475	2	T33979	hypothetical prote
39	412.5	14.9	537	2	T25536	hypothetical prote
40	411	14.8	745	2	T23893	hypothetical prote
41	409.5	14.8	661	2	T32518	hypothetical prote
42	408	14.7	533	2	T34457	hypothetical prote
43	405.5	14.6	520	2	T19661	hypothetical prote
44	405	14.6	530	2	T18596	hypothetical prote
45	398.5	14.4	526	2	T25535	hypothetical prote
46	398	14.4	534	2	T27588	hypothetical prote
47	392.5	14.2	529	2	T33738	hypothetical prote
48	391.5	14.1	530	2	T19365	hypothetical prote
49	391	14.1	537	2	T21823	hypothetical prote
50	389	14.1	531	2	T15329	hypothetical prote
51	387.5	14.0	504	2	T34106	hypothetical prote
52	386.5	14.0	542	2	T20457	hypothetical prote
53	384	13.9	417	2	T34459	hypothetical prote
54	383.5	13.9	567	2	T25771	hypothetical prote
55	382.5	13.8	574	2	T19738	hypothetical prote
56	380.5	13.7	535	2	T24309	hypothetical prote
57	379.5	13.7	535	2	T27582	hypothetical prote
58	377	13.6	540	2	T33982	hypothetical prote
59	375.5	13.6	525	2	T24647	hypothetical prote
60	375	13.5	522	2	T31893	hypothetical prote
61	374	13.5	526	2	T27581	hypothetical prote
62	373	13.5	611	2	T03890	hypothetical prote
63	364.5	13.2	1003	2	T19638	hypothetical prote
64	362	13.1	529	2	T18595	hypothetical prote
65	361.5	13.1	533	2	T27589	hypothetical prote
66	361.5	13.1	581	2	T33737	hypothetical prote
67	361	13.0	531	2	T25537	hypothetical prote
68	360.5	13.0	531	2	T33981	hypothetical prote
69	357	12.9	174	2	A47113	glucuronosyltransf
70	354.5	12.8	540	2	T20456	hypothetical prote

71	349.5	12.6	502	2	T25263	hypothetical prote
72	346.5	12.5	515	2	S52453	ecdysteroid UDP-gl
73	344	12.4	710	2	B89252	protein ZC455.4 [i
74	339	12.2	558	2	T15939	hypothetical prote
75	333	12.0	506	2	H88809	protein R11A8.3 [i
76	328	11.8	560	2	T30475	probable phenol be
77	326	11.8	515	2	T32217	hypothetical prote
78	322	11.6	540	2	T15573	hypothetical prote
79	317	11.5	514	2	T25534	hypothetical prote
80	317	11.5	593	2	T32485	hypothetical prote
81	309.5	11.2	579	2	H88632	protein F56B3.7 [i
82	309	11.2	523	2	T28727	hypothetical prote
83	305.5	11.0	440	2	T24478	hypothetical prote
84	300.5	10.9	542	2	T28719	hypothetical prote
85	292	10.5	435	2	T24477	hypothetical prote
86	288.5	10.4	572	2	T32303	hypothetical prote
87	280	10.1	523	2	T28721	hypothetical prote
88	274.5	9.9	580	2	T28725	hypothetical prote
89	272	9.8	534	2	T28720	hypothetical prote
90	270	9.8	405	2	G89075	protein K04A8.10 [
91	264.5	9.6	501	2	T31754	hypothetical prote
92	259.5	9.4	489	2	T10283	ecdysteroid UDPglu
93	257.5	9.3	495	2	T28722	hypothetical prote
94	257.5	9.3	703	2	S40710	hypothetical prote
95	256	9.2	310	2	G02309	UDP-glucuronosyltr
96	256	9.2	506	2	T33770	hypothetical prote
97	255	9.2	289	2	B42586	glucuronosyltransf
98	248	9.0	506	2	T41760	UDP-glucosyl trans
99	246.5	8.9	506	1	XUNVAC	ecdysteroid UDPglu
100	245.5	8.9	457	2	H89251	protein ZC455.6 [i
101	244.5	8.8	289	2	D42586	glucuronosyltransf
102	244	8.8	581	2	B87768	protein F54C1.1 [i
103	242.5	8.8	795	2	T20609	hypothetical prote
104	226	8.2	289	2	C42586	glucuronosyltransf
105	224.5	8.1	285	2	G02240	UDP-glucuronosyltr
106	197.5	7.1	488	2	T49903	glucosyltransferas
107	186	6.7	419	1	S74500	zeaxanthin glucosy
108	185.5	6.7	484	2	D71419	probable indole-3-
109	185	6.7	433	2	S51767	glycosyl transfera
110	184.5	6.7	453	2	A86191	hypothetical prote
111	182	6.6	413	2	S52980	zeaxanthin glucosy
112	181.5	6.6	449	2	H84870	probable glucosylt
113	181.5	6.6	479	2	E71419	probable indole-3-
114	180.5	6.5	260	2	T31894	hypothetical prote
115	178	6.4	428	2	C70670	probable glycosyl-
116	177	6.4	457	2	B84725	probable glucosylt
117	176.5	6.4	1184	2	H86190	hypothetical prote
118	175.5	6.3	480	2	B85014	probable flavonol
119	173.5	6.3	431	2	B37802	crtX protein - Erw
120	172	6.2	476	2	H86207	hypothetical prote
121	171	6.2	452	2	T00981	probable glucosylt
122	171	6.2	467	2	H84699	probable flavonol
123	169.5	6.1	459	2	T51558	probable flavonol
124	169.5	6.1	487	2	C86356	UDP-glucose glucos
125	169	6.1	456	2	T00506	indole-3-acetate b
126	168.5	6.1	456	2	F84724	probable glucosylt
127	167.5	6.1	475	2	F71419	probable indole-3-

128	166	6.0	460	2	T00639	hypothetical prote
129	165.5	6.0	407	2	T37104	probable glycosyl
130	165.5	6.0	462	2	T01732	UTP-glucose glucos
131	164.5	5.9	449	2	B84871	probable glucosylt
132	164.5	5.9	472	2	T51559	probable flavonol
133	164	5.9	471	2	A54739	indole-3-acetate b
134	164	5.9	478	2	T08395	UTP-glucose glucos
135	163.5	5.9	457	2	C85434	glucosyltransferas
136	163.5	5.9	471	2	S01052	flavonol 3-O-gluco
137	162.5	5.9	420	2	T08005	flavonol 3-O-gluco
138	162.5	5.9	453	2	T45603	glucosyltransferas
139	162	5.9	464	2	T47710	glucuronosyl trans
140	161	5.8	474	2	A84700	probable flavonol
141	161	5.8	1198	2	S51434	hypothetical prote
142	159.5	5.8	478	2	A71417	hypothetical prote
143	159	5.7	287	2	S41953	UTP-glucose glucos
144	159	5.7	460	2	T51560	probable flavonol
145	158.5	5.7	471	1	S08325	flavonol 3-O-gluco
146	158	5.7	496	2	E84784	probable glucosyl
147	157.5	5.7	435	2	H86924	probable glycosyl
148	157.5	5.7	467	2	F84699	probable flavonol
149	157.5	5.7	471	2	S01037	flavonol 3-O-gluco
150	157	5.7	317	2	T31897	hypothetical prote
151	156.5	5.7	442	2	F84618	probable flavonol
152	155.5	5.6	392	1	C69851	macrolide glycosyl
153	155	5.6	470	2	D84614	hypothetical prote
154	154.5	5.6	431	2	S52583	crtX protein - Erw
155	154	5.6	495	2	H84784	probable glucosyl
156	153.5	5.5	487	2	S41951	UTP-glucose glucos
157	153	5.5	451	2	T45604	glucosyltransferas
158	153	5.5	496	2	F84784	probable glucosyl
159	152.5	5.5	495	2	G84784	probable glucosyl
160	151.5	5.5	438	2	E86924	probable glycosyl
161	151.5	5.5	478	2	E84545	probable glucosylt
162	151	5.5	453	2	D86430	probable UDP-gulco
163	149.5	5.4	449	2	G70670	hypothetical prote
164	149.5	5.4	466	2	T07404	probable glucosylt
165	149.5	5.4	489	2	H86356	probable UDP-gluco
166	149	5.4	507	2	T46161	glucosyltransferas
167	148.5	5.4	347	2	T06371	probable UDP-glucu
168	148.5	5.4	438	2	T45602	glucosyltransferas
169	147.5	5.3	442	2	H85096	hypothetical prote
170	147.5	5.3	479	2	F86356	T16E15.2 protein -
171	147.5	5.3	481	2	B84700	probable flavonol
172	146.5	5.3	452	2	T12981	hypothetical prote
173	146.5	5.3	458	2	C71420	hypothetical prote
174	146.5	5.3	476	2	T03745	glucosyltransferas
175	146.5	5.3	496	2	D84784	probable glucosyl
176	146	5.3	452	2	G71416	probable glucosylt
177	146	5.3	491	2	C84784	probable glucosyl
178	145.5	5.3	481	2	G86144	hypothetical prote
179	145	5.2	453	2	T00511	indole-3-acetate b
180	144	5.2	407	2	C97234	probable glycosyl
181	143.5	5.2	479	2	G86207	hypothetical prote
182	143	5.2	469	2	D86144	protein probable U
183	143	5.2	481	2	E86356	hypothetical prote
184	142.5	5.1	472	2	S39507	glucuronosyl trans

185	142	5.1	424	2	T51110	glycosyltransferas
186	141.5	5.1	449	2	T45605	glucosyltransferas
187	141.5	5.1	476	2	T03747	glucosyltransferas
188	141	5.1	394	2	S41952	UTP-glucose glucos
189	141	5.1	481	2	T01850	UTP-glucose glucos
190	140.5	5.1	346	2	S41954	UTP-glucose glucos
191	140.5	5.1	486	2	T51431	glucosyltransferas
192	140	5.1	480	2	F86207	hypothetical prote
193	139.5	5.0	452	2	F96672	Similar to Flavono
194	138.5	5.0	444	2	G84565	probable flavonol
195	138.5	5.0	449	2	S41950	UTP-glucose glucos
196	138.5	5.0	450	2	D86356	hypothetical prote
197	138.5	5.0	460	2	T47709	glucuronosyl trans
198	138	5.0	385	2	T12980	hypothetical prote
199	138	5.0	438	2	T00507	indole-3-acetate b
200	138	5.0	455	2	T00584	indole-3-acetate b
201	137.5	5.0	467	2	T02238	glucosyl transfera
202	136.5	4.9	488	2	T07786	UDP-glucose glucos
203	135	4.9	470	2	H84565	probable flavonol
204	135	4.9	490	2	T46162	glucosyltransferas
205	134	4.8	455	2	T05861	hypothetical prote
206	134	4.8	456	2	C71402	probable glucosylt
207	133.5	4.8	398	2	A97146	probable glycosylt
208	132.5	4.8	447	2	T12978	hypothetical prote
209	132.5	4.8	447	2	E96672	Similar to Flavono
210	131.5	4.8	287	2	H69906	macrolide glycosyl
211	130.5	4.7	170	2	G86356	hypothetical prote
212	130	4.7	455	1	XUBHFG	flavonol 3-O-gluco
213	129.5	4.7	400	2	C97147	probable glycosylt
214	128.5	4.6	398	2	F64456	hypothetical prote
215	128.5	4.6	430	1	S33184	glycosyltransferas
216	126	4.6	440	2	T00583	probable indole-3-
217	125.5	4.5	381	1	A69784	macrolide glycosyl
218	120.5	4.4	490	2	H84786	probable glucosylt
219	120	4.3	418	2	F75587	probable glycosylt
220	118.5	4.3	418	2	JS0636	glycosyl transfera
221	118.5	4.3	453	2	T05862	hypothetical prote
222	115.5	4.2	433	2	H96549	hypothetical prote
223	115	4.2	615	2	D96499	probable UDP-gluco
224	114	4.1	1274	2	JN0015	trp protein - frui
225	113.5	4.1	460	2	F84529	probable glucosylt
226	113.5	4.1	473	2	S60290	anthocyanin rhamno
227	113	4.1	478	2	T05423	probable glucosylt
228	112.5	4.1	281	2	T29825	hypothetical prote
229	112.5	4.1	732	2	T14233	NADH2 dehydrogenas
230	111.5	4.0	374	2	C85609	probable glucosylt
231	111.5	4.0	374	2	B90800	probable glucosyl-
232	111.5	4.0	465	2	T48374	UDPG glucosyltrans
233	111.5	4.0	471	2	S36655	UDP rhamnose-antho
234	111	4.0	842	2	S56819	hypothetical prote
235	110.5	4.0	445	2	S75596	hypothetical prote
236	109.5	4.0	598	2	C97273	mutS-like mismatch
237	109.5	4.0	1221	2	T25005	hypothetical prote
238	109	3.9	408	2	T44859	glycosyltransferas
239	108.5	3.9	1232	2	D64413	cobalamin biosynth
240	108	3.9	3079	1	RGBYI2	probable GTPase-ac
241	107	3.9	427	2	G81260	UDP-N-acetylmuramo

242	106	3.8	388	2	B70878	probable transfera
243	106	3.8	482	2	E84680	probable glucosylt
244	105.5	3.8	484	2	E84529	probable glucosylt
245	105.5	3.8	556	2	S51858	probable membrane
246	105.5	3.8	570	2	D96766	protein glucosyltr
247	105.5	3.8	732	2	T13814	NADH2 dehydrogenas
248	105	3.8	408	2	T44860	glycosyltransferas
249	103.5	3.7	371	2	AC0837	probable glycosylt
250	103.5	3.7	371	2	T30292	glucosyl-transfera
251	103.5	3.7	448	2	C96542	hypothetical prote
252	103.5	3.7	469	1	RGKBCP	nitrogen regulatio
253	103.5	3.7	622	2	A45746	phosphoenolpyruvat
254	103	3.7	395	2	AB0242	probable glycosyl
255	103	3.7	508	2	S12640	transposition prot
256	103	3.7	967	2	A30325	membrane alanyl am
257	102.5	3.7	435	2	A86195	hypothetical prote
258	102.5	3.7	663	2	F90291	hypothetical prote
259	102.5	3.7	706	2	D90124	hypothetical prote
260	102.5	3.7	1275	2	JU0092	trp protein - frui
261	102	3.7	334	2	H75362	hypothetical prote
262	102	3.7	1655	2	S47446	nucleoporin Np188
263	101.5	3.7	385	2	C71699	murg protein (murG
264	101.5	3.7	728	2	T13794	NADH2 dehydrogenas
265	101	3.6	511	2	S43685	monoamine transpor
266	101	3.6	693	2	T13175	NADH2 dehydrogenas
267	101	3.6	697	2	T13754	NADH2 dehydrogenas
268	100.5	3.6	370	2	E96929	probable permease
269	100.5	3.6	740	2	T12753	NADH2 dehydrogenas
270	100.5	3.6	858	2	A44919	GCR3 protein - yea
271	100	3.6	1058	2	D82654	ankyrin-like prote
272	99.5	3.6	396	2	B69325	LPS biosynthesis p
273	99	3.6	190	2	T24652	hypothetical prote
274	99	3.6	686	2	T13561	NADH2 dehydrogenas
275	99	3.6	738	2	T12192	NADH2 dehydrogenas
276	98.5	3.6	733	2	T12220	NADH2 dehydrogenas
277	98.5	3.6	942	2	S75598	poly(A) polymerase
278	98.5	3.6	1049	2	S67613	vacuolar carboxype
279	98	3.5	382	2	T46519	probable glycosyl
280	98	3.5	622	1	QYCHGC	phosphoenolpyruvat
281	98	3.5	1271	2	T43269	microcystin synthe
282	97.5	3.5	387	2	A81324	cyclopropane-fatty
283	97.5	3.5	514	1	A44405	tyrosine decarboxy
284	97.5	3.5	774	2	S25284	protein kinase nek
285	97.5	3.5	1830	2	E82909	conserved hypothet
286	97	3.5	392	2	S72936	UDP-glucuronosyltr
287	97	3.5	664	2	A72215	excinuclease ABC c
288	96.5	3.5	358	2	D95041	hypothetical prote
289	96.5	3.5	383	2	AG2894	conserved hypothet
290	96.5	3.5	388	2	B97670	hypothetical prote
291	96.5	3.5	521	2	D75581	malate synthase -
292	96.5	3.5	612	2	G83307	hypothetical prote
293	96	3.5	336	2	C71154	hypothetical prote
294	96	3.5	544	2	S54531	hypothetical prote
295	95.5	3.5	469	2	S53024	nitrogen regulatio
296	95.5	3.5	505	2	T00400	hypothetical prote
297	95.5	3.5	698	2	T12586	NADH2 dehydrogenas
298	95.5	3.5	741	2	T12707	NADH2 dehydrogenas

299	95	3.4	204	2	E85660	hypothetical prote
300	95	3.4	470	2	AG0003	nitrogen regulatio
301	95	3.4	535	2	E86334	hypothetical prote
302	95	3.4	707	2	T12665	NADH2 dehydrogenas
303	95	3.4	707	2	T12751	NADH2 dehydrogenas
304	95	3.4	707	2	T12752	NADH2 dehydrogenas
305	94.5	3.4	282	2	AF2432	hypothetical prote
306	94.5	3.4	333	2	E97257	spore coat protein
307	94.5	3.4	427	2	G72278	hypothetical prote
308	94.5	3.4	705	2	T34477	hypothetical prote
309	94.5	3.4	705	2	A86497	conserved hypothet
310	94.5	3.4	705	2	F72125	conserved hypothet
311	94.5	3.4	741	2	T13791	NADH2 dehydrogenas
312	94	3.4	296	2	D48327	COI intron i3 prot
313	94	3.4	531	2	F70415	CTP synthetase - A
314	94	3.4	707	2	T12759	NADH2 dehydrogenas
315	94	3.4	707	2	T12658	NADH2 dehydrogenas
316	94	3.4	707	2	T12664	NADH2 dehydrogenas
317	93.5	3.4	411	2	T46681	probable glycosylt
318	93.5	3.4	681	2	T39814	hypothetical prote
319	93.5	3.4	731	2	T14231	NADH2 dehydrogenas
320	93.5	3.4	734	2	T13685	NADH2 dehydrogenas
321	93.5	3.4	763	2	H70145	ATP-dependent Clp
322	93.5	3.4	1032	2	D95177	Snf2 family protei
323	93.5	3.4	1169	2	H70178	exodeoxyribonuclea
324	93.5	3.4	1203	2	T28895	hypothetical prote
325	93.5	3.4	1826	2	H86502	excinnuclease ABC s
326	93.5	3.4	1826	2	D72120	excinnuclease ABC,
327	93	3.4	700	2	T12589	NADH2 dehydrogenas
328	93	3.4	707	2	T12668	NADH2 dehydrogenas
329	93	3.4	707	2	T12671	NADH2 dehydrogenas
330	93	3.4	707	2	T13036	NADH2 dehydrogenas
331	93	3.4	707	2	T13032	NADH2 dehydrogenas
332	93	3.4	737	2	T14232	NADH2 dehydrogenas
333	92.5	3.3	460	2	B48057	farnesyl-diphospha
334	92.5	3.3	460	2	T40581	farnesyl-diphospha
335	92.5	3.3	469	2	AC0950	Two-component syst
336	92.5	3.3	562	2	T34319	hypothetical prote
337	92.5	3.3	622	1	QYRTGP	phosphoenolpyruvat
338	92.5	3.3	727	2	T12221	NADH2 dehydrogenas
339	92.5	3.3	828	2	JC5807	trp3 protein - rat
340	92	3.3	402	2	AE2894	conserved hypothet
341	92	3.3	405	2	H97669	hypothetical prote
342	92	3.3	468	1	RGECGG	nitrogen regulatio
343	92	3.3	514	1	ALBSN	alpha-amylase (EC
344	92	3.3	586	2	JC5618	beta-galactosidase
345	92	3.3	697	2	T13662	NADH2 dehydrogenas
346	92	3.3	1442	2	C82898	DNA polymerase III
347	91.5	3.3	550	2	B82330	glucose-6-phosphat
348	91.5	3.3	593	2	S17433	auxin-regulated pr
349	91.5	3.3	602	2	S69198	prostaglandin G/H
350	91.5	3.3	645	2	T12159	NADH2 dehydrogenas
351	91.5	3.3	661	2	T13761	NADH2 dehydrogenas
352	91.5	3.3	696	2	T12160	NADH2 dehydrogenas
353	91.5	3.3	732	2	T12194	NADH2 dehydrogenas
354	91.5	3.3	737	2	T12193	NADH2 dehydrogenas
355	91.5	3.3	744	2	T13485	NADH2 dehydrogenas

356	91.5	3.3	1032	2	F98043	SWF/SNF family ATP
357	91.5	3.3	1121	2	C82120	transcription regu
358	91.5	3.3	1199	2	G69698	RNA polymerase (be
359	91	3.3	364	2	D95116	ferrochelataase [im
360	91	3.3	364	2	B97986	ferrochelataase (EC
361	91	3.3	688	2	T13248	NADH2 dehydrogenas
362	91	3.3	698	2	T12563	NADH2 dehydrogenas
363	91	3.3	733	2	T12213	NADH2 dehydrogenas
364	91	3.3	736	2	T12218	NADH2 dehydrogenas
365	91	3.3	755	2	T15791	hypothetical prote
366	91	3.3	757	2	T34362	hypothetical prote
367	90.5	3.3	346	2	G69325	LPS glycosyltransf
368	90.5	3.3	381	2	F71196	probable hexosyltr
369	90.5	3.3	602	2	A35564	prostaglandin-endo
370	90.5	3.3	734	2	T12602	NADH2 dehydrogenas
371	90.5	3.3	741	2	T12642	NADH2 dehydrogenas
372	90.5	3.3	749	2	T13034	NADH2 dehydrogenas
373	90.5	3.3	2783	2	T34416	hypothetical prote
374	90	3.3	356	2	G72386	conserved hypothet
375	90	3.3	479	2	C75099	hypothetical prote
376	90	3.3	480	2	T34294	hypothetical prote
377	90	3.3	557	2	H72400	excinuclease ABC c
378	90	3.3	665	2	T13488	NADH2 dehydrogenas
379	90	3.3	683	2	T12153	NADH2 dehydrogenas
380	90	3.3	688	2	T13249	NADH2 dehydrogenas
381	90	3.3	699	2	T12667	NADH2 dehydrogenas
382	90	3.3	699	2	T12673	NADH2 dehydrogenas
383	90	3.3	702	2	T13058	NADH2 dehydrogenas
384	90	3.3	817	2	D86217	protein T27G7.8 [i
385	90	3.3	1157	2	A55152	PAS1 protein - yea
386	90	3.3	1953	2	S63244	BNI1 protein - yea
387	89.5	3.2	274	1	D70378	conserved hypothet
388	89.5	3.2	289	2	T34454	hypothetical prote
389	89.5	3.2	422	2	C71930	udp-n-acetylmuramo
390	89.5	3.2	468	2	F84686	hypothetical prote
391	89.5	3.2	500	2	I56601	cytochrome P450 al
392	89.5	3.2	580	2	T31529	hypothetical prote
393	89.5	3.2	657	2	E81119	tail fibre protein
394	89.5	3.2	657	2	E81901	probable phage tai
395	89.5	3.2	744	2	T12758	NADH2 dehydrogenas
396	89.5	3.2	930	2	E98059	isoleucine-tRNA li
397	89.5	3.2	3268	2	S69625	hypothetical prote
398	89	3.2	276	2	B86710	intercellular adhe
399	89	3.2	298	2	A75119	hypothetical prote
400	89	3.2	377	2	T46149	protein kinase ATN
401	89	3.2	431	2	I40898	3-deoxy-manno-octu
402	89	3.2	686	2	T13234	NADH2 dehydrogenas
403	89	3.2	686	2	T13252	NADH2 dehydrogenas
404	89	3.2	686	2	T13768	NADH2 dehydrogenas
405	89	3.2	686	2	T13490	NADH2 dehydrogenas
406	89	3.2	686	2	T13766	NADH2 dehydrogenas
407	89	3.2	688	2	T13282	NADH2 dehydrogenas
408	89	3.2	688	2	T13278	NADH2 dehydrogenas
409	89	3.2	688	2	T13242	NADH2 dehydrogenas
410	89	3.2	688	2	T13373	NADH2 dehydrogenas
411	89	3.2	688	2	T13243	NADH2 dehydrogenas
412	89	3.2	688	2	T13253	NADH2 dehydrogenas

413	89	3.2	688	2	T12670	NADH2 dehydrogenas
414	89	3.2	696	2	T12659	NADH2 dehydrogenas
415	89	3.2	990	2	D83706	lantibiotic mersac
416	89	3.2	1058	2	T19282	hypothetical prote
417	89	3.2	3147	2	T21328	hypothetical prote
418	88.5	3.2	252	2	S50806	hypothetical prote
419	88.5	3.2	396	2	A59226	tauropine dehydrog
420	88.5	3.2	425	2	H90415	hypothetical prote
421	88.5	3.2	500	1	DCJAAP	aromatic-L-amino-a
422	88.5	3.2	647	1	QYFFGM	phosphoenolpyruvat
423	88.5	3.2	721	2	T12212	NADH2 dehydrogenas
424	88.5	3.2	737	2	T13504	NADH2 dehydrogenas
425	88.5	3.2	741	2	T13361	NADH2 dehydrogenas
426	88.5	3.2	741	2	T13774	NADH2 dehydrogenas
427	88.5	3.2	899	2	H96617	probable disease r
428	88.5	3.2	1435	2	D96693	protein Putative A
429	88.5	3.2	1561	1	C69145	protoporphyrin IX
430	88.5	3.2	1640	2	H88094	protein F39E9.2 [i
431	88	3.2	405	2	D82542	two-component syst
432	88	3.2	431	2	S41168	3-deoxy-manno-octu
433	88	3.2	431	2	I40897	3-deoxy-manno-octu
434	88	3.2	628	2	S51422	probable membrane
435	88	3.2	694	2	T12712	NADH2 dehydrogenas
436	88	3.2	694	2	T12675	NADH2 dehydrogenas
437	88	3.2	698	2	T12588	NADH2 dehydrogenas
438	88	3.2	699	2	T17119	NADH2 dehydrogenas
439	88	3.2	729	2	T12227	NADH2 dehydrogenas
440	88	3.2	731	2	T12226	NADH2 dehydrogenas
441	88	3.2	1244	2	C96584	hypothetical prote
442	88	3.2	5138	2	B96695	hypothetical prote
443	87.5	3.2	399	2	G70328	chromosome replica
444	87.5	3.2	412	2	JC1452	translation initia
445	87.5	3.2	432	2	A64602	processing protein
446	87.5	3.2	447	2	B98052	conserved hypothet
447	87.5	3.2	472	2	G81293	probable type II p
448	87.5	3.2	509	2	T00793	hypothetical prote
449	87.5	3.2	578	2	D89772	hypothetical prote
450	87.5	3.2	635	2	T46407	probable RNA helic
451	87.5	3.2	673	2	T20936	hypothetical prote
452	87.5	3.2	744	2	T13040	NADH2 dehydrogenas
453	87.5	3.2	749	2	JC7729	replication protei
454	87.5	3.2	995	2	T27327	hypothetical prote
455	87.5	3.2	1377	2	T19214	UDP-glucose-glycop
456	87.5	3.2	1452	1	S17669	protein-tyrosine-p
457	87.5	3.2	1597	2	S55144	RLR1 protein - yea
458	87.5	3.2	1830	1	S19188	myosin-V - chicken
459	87	3.1	141	2	T10306	hypothetical prote
460	87	3.1	214	2	T49174	hypothetical prote
461	87	3.1	333	2	AF2124	hypothetical prote
462	87	3.1	412	2	T47321	hypothetical prote
463	87	3.1	430	2	F81698	3-deoxy-manno-octu
464	87	3.1	431	2	I40894	3-deoxy-manno-octu
465	87	3.1	500	2	T33279	hypothetical prote
466	87	3.1	511	2	S43686	monoamine transpor
467	87	3.1	512	2	C64599	hypothetical prote
468	87	3.1	551	2	T50663	RCC1-like G exchan
469	87	3.1	661	2	F90360	hypothetical prote

470	87	3.1	684	2	T12151	NADH2 dehydrogenas
471	87	3.1	694	2	T13573	NADH2 dehydrogenas
472	87	3.1	698	2	T12562	NADH2 dehydrogenas
473	87	3.1	734	1	DERZN5	NADH2 dehydrogenas
474	87	3.1	736	2	T12217	NADH2 dehydrogenas
475	87	3.1	839	2	S73548	MG422 homolog C12_
476	87	3.1	1037	2	T18365	polysialyltransfer
477	87	3.1	1037	2	T18368	polysialyltransfer
478	87	3.1	1167	2	F71909	hypothetical prote
479	87	3.1	1411	2	S55123	hypothetical prote
480	87	3.1	1581	2	T30832	pentafunctional en
481	87	3.1	1828	2	B59254	myosin heavy chain
482	87	3.1	1853	1	A46761	myosin heavy chain
483	87	3.1	1855	2	A59254	myosin heavy chain
484	87	3.1	4717	2	T41581	hypothetical coile
485	86.5	3.1	316	2	C96020	probable sugar upt
486	86.5	3.1	358	2	AB2041	hypothetical prote
487	86.5	3.1	359	2	A97175	undecaprenyl-PP-Mu
488	86.5	3.1	376	2	AG2227	DNA repair and gen
489	86.5	3.1	409	2	F71956	hypothetical prote
490	86.5	3.1	413	2	D72279	conserved hypothet
491	86.5	3.1	417	2	F96607	probable clathrin-
492	86.5	3.1	469	2	E86074	hypothetical prote
493	86.5	3.1	469	2	F91227	response regulator
494	86.5	3.1	495	2	T46700	hypothetical prote
495	86.5	3.1	563	2	T44214	probable phosphotr
496	86.5	3.1	617	2	S37744	endo-exonuclease y
497	86.5	3.1	622	2	JC7973	synleurin - human
498	86.5	3.1	682	2	T12715	NADH2 dehydrogenas
499	86.5	3.1	733	2	T22011	hypothetical prote
500	86.5	3.1	741	2	T12691	NADH2 dehydrogenas
501	86.5	3.1	741	2	T12762	NADH2 dehydrogenas
502	86.5	3.1	741	2	T13372	NADH2 dehydrogenas
503	86.5	3.1	741	2	T13509	NADH2 dehydrogenas
504	86.5	3.1	741	2	T13765	NADH2 dehydrogenas
505	86.5	3.1	744	2	T12627	NADH2 dehydrogenas
506	86.5	3.1	744	2	T13585	NADH2 dehydrogenas
507	86.5	3.1	747	2	T13683	NADH2 dehydrogenas
508	86.5	3.1	892	2	AE0650	alcohol dehydrogen
509	86.5	3.1	1076	2	A69409	carbamoyl-phosphat
510	86.5	3.1	1575	2	S68448	synaptojanin, 170K
511	86.5	3.1	1702	2	S42459	DNA-directed DNA p
512	86	3.1	342	2	T48045	hypothetical prote
513	86	3.1	410	2	A64234	ATP-dependent RNA
514	86	3.1	649	1	TVVPMK	large T antigen -
515	86	3.1	684	2	T13491	NADH2 dehydrogenas
516	86	3.1	700	2	T13763	NADH2 dehydrogenas
517	86	3.1	703	2	T13074	NADH2 dehydrogenas
518	86	3.1	706	2	A48084	STE11 protein kina
519	86	3.1	713	2	JC2534	RVLG protein - rat
520	86	3.1	746	2	S08494	NADH2 dehydrogenas
521	86	3.1	881	2	S67026	probable membrane
522	86	3.1	891	1	DEEC	acetaldehyde dehyd
523	86	3.1	891	2	D85704	hypothetical prote
524	86	3.1	891	2	E90846	acetaldehyde dehyd
525	86	3.1	1025	2	H81751	exodeoxyribonuclea
526	86	3.1	3194	2	D71917	toxin-like outer m

527	86	3.1	5175	2	T20992	hypothetical prote
528	86	3.1	5198	2	T43290	hemicentin precurs
529	85.5	3.1	332	2	T32852	hypothetical prote
530	85.5	3.1	338	2	G97771	capM protein [impo
531	85.5	3.1	352	2	D97947	UDP-N-acetylglucos
532	85.5	3.1	356	2	H81800	conserved hypothet
533	85.5	3.1	356	2	F81068	conserved hypothet
534	85.5	3.1	406	2	C72340	probable hexosyltr
535	85.5	3.1	467	2	AG0546	probable terminal
536	85.5	3.1	469	2	B70486	hypothetical prote
537	85.5	3.1	491	2	C86781	alpha-amylase [imp
538	85.5	3.1	492	2	S32491	testosterone 7alph
539	85.5	3.1	494	2	B89870	hypothetical prote
540	85.5	3.1	506	2	F83545	hypothetical prote
541	85.5	3.1	546	2	D89813	alpha-glucosidase
542	85.5	3.1	557	2	E83744	hypothetical prote
543	85.5	3.1	677	2	F64139	guanosine-3',5'-bi
544	85.5	3.1	681	2	T13566	NADH2 dehydrogenas
545	85.5	3.1	702	2	T13708	NADH2 dehydrogenas
546	85.5	3.1	731	2	T16524	hypothetical prote
547	85.5	3.1	740	1	DENTN5	NADH2 dehydrogenas
548	85.5	3.1	741	2	T12711	NADH2 dehydrogenas
549	85.5	3.1	741	2	T13054	NADH2 dehydrogenas
550	85.5	3.1	741	2	T13508	NADH2 dehydrogenas
551	85.5	3.1	741	2	T13776	NADH2 dehydrogenas
552	85.5	3.1	741	2	T12692	NADH2 dehydrogenas
553	85.5	3.1	741	2	T12706	NADH2 dehydrogenas
554	85.5	3.1	741	2	T13042	NADH2 dehydrogenas
555	85.5	3.1	741	2	T13247	NADH2 dehydrogenas
556	85.5	3.1	741	2	T13398	NADH2 dehydrogenas
557	85.5	3.1	743	2	T12626	NADH2 dehydrogenas
558	85.5	3.1	743	2	T13238	NADH2 dehydrogenas
559	85.5	3.1	744	2	T12603	NADH2 dehydrogenas
560	85.5	3.1	744	2	T13755	NADH2 dehydrogenas
561	85.5	3.1	749	2	T12623	NADH2 dehydrogenas
562	85.5	3.1	891	2	AG0265	alcohol dehydrogen
563	85.5	3.1	1173	2	T42719	TPR-containing/SH2
564	85	3.1	180	2	AF1175	transcription regu
565	85	3.1	185	2	A82569	hypoxanthine-guani
566	85	3.1	217	2	H90143	hypothetical prote
567	85	3.1	283	2	T27423	hypothetical prote
568	85	3.1	418	2	G75496	UDP-N-acetylglucos
569	85	3.1	458	2	F84746	probable serine ca
570	85	3.1	542	2	JN0438	carboxylesterase (
571	85	3.1	584	2	T14631	glucose-6-phosphat
572	85	3.1	614	2	T29937	hypothetical prote
573	85	3.1	656	2	A96724	hypothetical prote
574	85	3.1	696	2	T12663	NADH2 dehydrogenas
575	85	3.1	698	2	T12560	NADH2 dehydrogenas
576	85	3.1	699	2	T12163	NADH2 dehydrogenas
577	85	3.1	699	2	T12169	NADH2 dehydrogenas
578	85	3.1	699	2	T12167	NADH2 dehydrogenas
579	85	3.1	699	2	T12172	NADH2 dehydrogenas
580	85	3.1	699	2	T12164	NADH2 dehydrogenas
581	85	3.1	699	2	T12168	NADH2 dehydrogenas
582	85	3.1	700	2	T13668	NADH2 dehydrogenas
583	85	3.1	700	2	T13702	NADH2 dehydrogenas

584	85	3.1	701	2	T13056	NADH2 dehydrogenas
585	85	3.1	705	2	T13494	NADH2 dehydrogenas
586	85	3.1	721	2	T14229	NADH2 dehydrogenas
587	85	3.1	736	2	T12225	NADH2 dehydrogenas
588	85	3.1	752	2	H86770	hypothetical prote
589	85	3.1	756	2	T05829	hypothetical prote
590	85	3.1	779	2	B81287	hypothetical prote
591	85	3.1	824	2	B38423	protein-glutamine
592	85	3.1	893	2	E72232	DNA-directed DNA p
593	85	3.1	988	2	E96621	hypothetical prote
594	85	3.1	1039	2	T28644	Y4jQ protein - Rhi
595	85	3.1	1045	2	E90705	hypothetical prote
596	85	3.1	1045	2	H85555	hypothetical prote
597	85	3.1	1058	2	S08436	pol polyprotein -
598	85	3.1	1238	2	T15824	hypothetical prote
599	85	3.1	1721	1	I38902	retinoblastoma bin
600	84.5	3.1	221	2	D70243	hypothetical prote
601	84.5	3.1	352	2	A95080	hypothetical prote
602	84.5	3.1	409	2	C64553	chlorohydrolase -
603	84.5	3.1	428	2	A30108	cyclin B - Atlanti
604	84.5	3.1	447	2	B95185	Mur ligase family
605	84.5	3.1	471	1	A44872	6-phosphofructo-2-
606	84.5	3.1	471	1	S12732	6-phosphofructo-2-
607	84.5	3.1	558	2	C88996	protein C17B7.8 [i
608	84.5	3.1	563	2	T44029	ganciclovir kinase
609	84.5	3.1	580	2	C81352	lipid export ABC t
610	84.5	3.1	738	2	S58612	NADH2 dehydrogenas
611	84.5	3.1	741	2	T13760	NADH2 dehydrogenas
612	84.5	3.1	741	2	T13658	NADH2 dehydrogenas
613	84.5	3.1	741	2	T13677	NADH2 dehydrogenas
614	84.5	3.1	742	2	T13245	NADH2 dehydrogenas
615	84.5	3.1	742	2	T13369	NADH2 dehydrogenas
616	84.5	3.1	743	2	T12690	NADH2 dehydrogenas
617	84.5	3.1	744	2	T13063	NADH2 dehydrogenas
618	84.5	3.1	744	2	T12694	NADH2 dehydrogenas
619	84.5	3.1	744	2	T12611	NADH2 dehydrogenas
620	84.5	3.1	744	2	T12761	NADH2 dehydrogenas
621	84.5	3.1	745	2	T12189	NADH2 dehydrogenas
622	84.5	3.1	822	2	B97839	ATP-dependent heli
623	84.5	3.1	850	2	A84685	probable RNA methy
624	84.5	3.1	940	2	B81852	probable type III
625	84.5	3.1	941	2	T49136	protein kinase-lik
626	84.5	3.1	1452	1	S17670	protein-tyrosine-p
627	84.5	3.1	1939	2	T18372	repeat organellar
628	84.5	3.1	3071	2	T50345	vacuolar protein s
629	84	3.0	292	2	H70313	cobalamin synthesi
630	84	3.0	345	2	B83260	probable transcrip
631	84	3.0	446	2	S34570	beta-glucosidase (
632	84	3.0	504	2	AC1740	S. pyogenes RofA r
633	84	3.0	525	2	T25550	hypothetical prote
634	84	3.0	600	2	T24626	hypothetical prote
635	84	3.0	621	2	T47843	dynamain-like prote
636	84	3.0	686	2	T13680	NADH2 dehydrogenas
637	84	3.0	686	2	T13235	NADH2 dehydrogenas
638	84	3.0	688	2	T13237	NADH2 dehydrogenas
639	84	3.0	689	2	T13771	NADH2 dehydrogenas
640	84	3.0	692	2	T12587	NADH2 dehydrogenas

641	84	3.0	696	2	T13767	NADH2 dehydrogenas
642	84	3.0	698	2	T12556	NADH2 dehydrogenas
643	84	3.0	741	2	T13086	NADH2 dehydrogenas
644	84	3.0	778	2	D72421	xylosidase - Therm
645	84	3.0	805	2	S07099	membrane alanyl am
646	84	3.0	950	2	A71655	hypothetical prote
647	84	3.0	1122	2	S64443	probable membrane
648	84	3.0	1171	2	G97174	pyruvate:ferredoxi
649	84	3.0	1219	2	H84464	probable helicase
650	84	3.0	1254	2	S46636	hypothetical prote
651	84	3.0	1311	2	T08986	hypothetical prote
652	84	3.0	1630	2	S64403	ESP1 protein - yea
653	84	3.0	1683	2	S56811	probable membrane
654	84	3.0	1966	2	T08991	hypothetical prote
655	83.5	3.0	261	2	F71693	probable enoyl-[ac
656	83.5	3.0	275	2	C81700	3-deoxy-manno-octu
657	83.5	3.0	305	2	D97169	uncharacterized pr
658	83.5	3.0	365	2	S54049	hypothetical prote
659	83.5	3.0	393	2	G83749	methionine gamma l
660	83.5	3.0	395	2	D89986	hypothetical prote
661	83.5	3.0	411	2	G75150	3-hydroxy-3-methyl
662	83.5	3.0	429	2	B97500	ribonuclease D (PA
663	83.5	3.0	544	2	AI3266	integral membrane
664	83.5	3.0	554	1	ZABPG4	replication initia
665	83.5	3.0	574	2	S45754	probable membrane
666	83.5	3.0	585	2	G86200	protein F12K11.15
667	83.5	3.0	602	2	S71557	pyruvate decarboxy
668	83.5	3.0	685	2	T12145	NADH2 dehydrogenas
669	83.5	3.0	697	2	T13370	NADH2 dehydrogenas
670	83.5	3.0	702	2	T13409	NADH2 dehydrogenas
671	83.5	3.0	703	2	T13696	NADH2 dehydrogenas
672	83.5	3.0	717	2	S23098	guanylate cyclase
673	83.5	3.0	738	2	T13406	NADH2 dehydrogenas
674	83.5	3.0	741	2	T13251	NADH2 dehydrogenas
675	83.5	3.0	741	2	T13697	NADH2 dehydrogenas
676	83.5	3.0	741	2	T13377	NADH2 dehydrogenas
677	83.5	3.0	741	2	T13706	NADH2 dehydrogenas
678	83.5	3.0	743	2	T12760	NADH2 dehydrogenas
679	83.5	3.0	744	2	T13043	NADH2 dehydrogenas
680	83.5	3.0	744	2	T13682	NADH2 dehydrogenas
681	83.5	3.0	930	2	A95193	isoleucyl-tRNA syn
682	83.5	3.0	1115	2	S57726	PAT1 protein - sli
683	83.5	3.0	1127	2	T03105	major single-stran
684	83.5	3.0	1133	2	JT0665	helicase II-like p
685	83.5	3.0	1157	2	AD1728	ATP-dependent deox
686	83.5	3.0	1181	2	T20386	hypothetical prote
687	83.5	3.0	1502	2	S45429	probable membrane
688	83.5	3.0	2265	2	T26183	hypothetical prote
689	83	3.0	180	2	AD1532	transcription regu
690	83	3.0	357	2	A65163	lipopolysaccharide
691	83	3.0	431	2	F96764	hypothetical prote
692	83	3.0	450	2	T39088	probable vacuolar
693	83	3.0	499	2	T45946	probable protein-k
694	83	3.0	516	2	T27092	hypothetical prote
695	83	3.0	577	2	T43207	nuclear fusion pro
696	83	3.0	590	2	T48625	pescadillo-like pr
697	83	3.0	592	2	T48155	pyruvate decarboxy

698	83	3.0	604	2	F89453	protein F35H12.4 [
699	83	3.0	652	2	T38704	glycyl tRNA synthe
700	83	3.0	688	2	T09604	NADH2 dehydrogenas
701	83	3.0	688	2	T09836	NADH2 dehydrogenas
702	83	3.0	689	2	T13762	NADH2 dehydrogenas
703	83	3.0	691	2	T12293	NADH2 dehydrogenas
704	83	3.0	698	2	T12565	NADH2 dehydrogenas
705	83	3.0	699	2	T12170	NADH2 dehydrogenas
706	83	3.0	699	2	T12173	NADH2 dehydrogenas
707	83	3.0	700	2	T12162	NADH2 dehydrogenas
708	83	3.0	731	2	T31914	hypothetical prote
709	83	3.0	736	2	T12222	NADH2 dehydrogenas
710	83	3.0	746	2	S71892	RNA-directed DNA p
711	83	3.0	774	2	D97527	omp1 protein precu
712	83	3.0	774	2	AE2746	group 1 outer memb
713	83	3.0	864	2	D70183	chemotaxis histidi
714	83	3.0	893	2	F86476	protein F15O4.39 [
715	83	3.0	1328	2	S78457	exonuclease II - f
716	83	3.0	1357	2	S57052	hypothetical prote
717	83	3.0	4924	2	T50176	probable peptide s
718	82.5	3.0	297	2	AC1494	transcription regu
719	82.5	3.0	335	2	A70128	conserved hypothet
720	82.5	3.0	356	2	B89919	hypothetical prote
721	82.5	3.0	385	2	S49111	peptide synthetase
722	82.5	3.0	426	2	C83212	rhamnosyltransfera
723	82.5	3.0	426	2	B53652	rhamnosyltransfera
724	82.5	3.0	443	2	T21598	hypothetical prote
725	82.5	3.0	456	2	C48572	rhopty protein ho
726	82.5	3.0	506	2	T29968	hypothetical prote
727	82.5	3.0	540	2	A82083	conserved hypothet
728	82.5	3.0	603	2	T03295	pyruvate decarboxy
729	82.5	3.0	625	2	F81287	probable sugar tra
730	82.5	3.0	684	2	T12124	NADH2 dehydrogenas
731	82.5	3.0	724	2	C83706	lantibiotic mersac
732	82.5	3.0	729	1	VCLJKX	env polyprotein pr
733	82.5	3.0	730	2	T13792	NADH2 dehydrogenas
734	82.5	3.0	732	2	T17469	NADH2 dehydrogenas
735	82.5	3.0	738	2	T13396	NADH2 dehydrogenas
736	82.5	3.0	741	2	T13404	NADH2 dehydrogenas
737	82.5	3.0	741	2	T12757	NADH2 dehydrogenas
738	82.5	3.0	741	2	T13378	NADH2 dehydrogenas
739	82.5	3.0	744	2	T13493	NADH2 dehydrogenas
740	82.5	3.0	848	2	A54740	interleukin-4-indu
741	82.5	3.0	861	1	VCLJKB	env polyprotein pr
742	82.5	3.0	926	2	AG1860	hypothetical prote
743	82.5	3.0	968	2	B64385	maltT-glpR intergen
744	82.5	3.0	975	2	A86258	protein F5O11.4 [i
745	82.5	3.0	1097	2	A29943	Toll protein precu
746	82.5	3.0	1098	2	JQ2209	helicase homolog g
747	82.5	3.0	1120	2	H71664	transcription-repa
748	82.5	3.0	1124	2	S06856	phytochrome - gard
749	82.5	3.0	1291	2	T22382	hypothetical prote
750	82.5	3.0	1335	2	T18289	racGAP protein - s
751	82.5	3.0	4452	1	YGBSG2	gramicidin S synth
752	82	3.0	54	2	A46292	zeaxanthin glucosy
753	82	3.0	319	2	S74012	hypothetical prote
754	82	3.0	321	2	E97584	hypothetical prote

755	82	3.0	388	2	F89773	hypothetical prote
756	82	3.0	413	2	S52020	translation initia
757	82	3.0	436	2	T38812	hypothetical prote
758	82	3.0	437	2	T48035	hypothetical prote
759	82	3.0	437	2	T39592	phosphatidylserine
760	82	3.0	442	2	D72498	probable serine hy
761	82	3.0	462	2	JC7805	toxin-A - Chiropsa
762	82	3.0	517	2	F64560	CMP-N-acetylneuram
763	82	3.0	535	2	A71319	probable glucose-6
764	82	3.0	539	2	T32052	hypothetical prote
765	82	3.0	553	2	C81024	hypothetical prote
766	82	3.0	574	2	A86255	hypothetical prote
767	82	3.0	602	2	S72513	FOG2 protein - yea
768	82	3.0	646	2	B70396	histidine kinase s
769	82	3.0	683	2	T12295	NADH2 dehydrogenas
770	82	3.0	684	2	T13695	NADH2 dehydrogenas
771	82	3.0	690	2	T12763	NADH2 dehydrogenas
772	82	3.0	710	2	T12143	NADH2 dehydrogenas
773	82	3.0	714	2	G86844	hypothetical prote
774	82	3.0	741	2	T12422	NADH2 dehydrogenas
775	82	3.0	883	2	T23948	hypothetical prote
776	82	3.0	913	2	T31497	hypothetical prote
777	82	3.0	964	2	G96662	probable aminopept
778	82	3.0	1005	2	F90099	hypothetical prote
779	82	3.0	1022	2	S50534	hypothetical prote
780	82	3.0	1024	2	G72041	exodeoxyribonuclea
781	82	3.0	1024	2	F86582	exodeoxyribonuclea
782	82	3.0	1024	2	D81624	exodeoxyribonuclea
783	82	3.0	1047	2	E64790	ybdE protein - Esc
784	82	3.0	1526	2	T41522	myosin ii - fissio
785	82	3.0	1957	2	T38077	hypothetical coile
786	82	3.0	3005	1	GNVSTV	genome polyprotein
787	81.5	2.9	305	2	T32235	hypothetical prote
788	81.5	2.9	306	2	G96935	mccF-like protein
789	81.5	2.9	341	2	E71191	probable 3-hydroxy
790	81.5	2.9	360	2	C72356	hypothetical prote
791	81.5	2.9	370	2	D83793	hypothetical prote
792	81.5	2.9	418	2	B72245	conserved hypothet
793	81.5	2.9	421	2	S73010	hypothetical prote
794	81.5	2.9	426	2	F70723	probable transfera
795	81.5	2.9	429	2	E84952	threonine synthase
796	81.5	2.9	473	2	T24686	hypothetical prote
797	81.5	2.9	479	1	A59380	protein kinase (EC
798	81.5	2.9	525	2	T41427	membrane transport
799	81.5	2.9	544	2	T51162	aminoglycoside ace
800	81.5	2.9	572	2	T51525	hypothetical prote
801	81.5	2.9	602	2	S39782	cyclooxygenase 1 -
802	81.5	2.9	623	2	G72412	hypothetical prote
803	81.5	2.9	638	2	H83905	hypothetical prote
804	81.5	2.9	697	2	T39512	hypothetical prote
805	81.5	2.9	698	2	T13657	NADH2 dehydrogenas
806	81.5	2.9	715	2	S77439	hypothetical prote
807	81.5	2.9	717	1	VGBE11	glycoprotein H pre
808	81.5	2.9	739	2	JS0675	vascular cell adhe
809	81.5	2.9	741	2	T12610	NADH2 dehydrogenas
810	81.5	2.9	741	2	T13085	NADH2 dehydrogenas
811	81.5	2.9	741	2	T12699	NADH2 dehydrogenas

812	81.5	2.9	741	2	T13051	NADH2 dehydrogenas
813	81.5	2.9	741	2	T13233	NADH2 dehydrogenas
814	81.5	2.9	741	2	T13569	NADH2 dehydrogenas
815	81.5	2.9	741	2	T13777	NADH2 dehydrogenas
816	81.5	2.9	744	2	G90124	hypothetical prote
817	81.5	2.9	794	2	S64362	probable membrane
818	81.5	2.9	825	2	T23612	hypothetical prote
819	81.5	2.9	836	2	A54269	protein-glutamine
820	81.5	2.9	1161	2	B86368	protein F28C11.9 [
821	81.5	2.9	1522	2	S48904	probable purine nu
822	81.5	2.9	1545	1	S71841	multidrug resistan
823	81	2.9	296	2	E71118	hypothetical prote
824	81	2.9	299	2	H90033	hypothetical prote
825	81	2.9	355	2	S52022	translation initia
826	81	2.9	364	2	S44899	ZK1236.4 protein -
827	81	2.9	413	2	S52017	translation initia
828	81	2.9	473	2	A56377	rubber particle cy
829	81	2.9	492	2	T38093	probable protein d
830	81	2.9	503	2	S14275	steroid 6beta-mono
831	81	2.9	509	2	T37587	hypothetical trp-a
832	81	2.9	532	2	S54571	probable membrane
833	81	2.9	541	2	A70141	oligopeptide ABC t
834	81	2.9	554	2	T13500	NADH2 dehydrogenas
835	81	2.9	649	2	T45102	H+-transporting tw
836	81	2.9	688	2	T48796	probable ATP-depen
837	81	2.9	689	2	T13280	NADH2 dehydrogenas
838	81	2.9	698	2	T30948	hypothetical prote
839	81	2.9	700	2	T13726	NADH2 dehydrogenas
840	81	2.9	701	2	T12296	NADH2 dehydrogenas
841	81	2.9	704	2	T13581	NADH2 dehydrogenas
842	81	2.9	726	2	T12215	NADH2 dehydrogenas
843	81	2.9	797	2	A70453	glutamate ammonia
844	81	2.9	807	2	S51460	hypothetical prote
845	81	2.9	820	2	T46412	ubiquitin-protein
846	81	2.9	894	2	D82127	alcohol dehydrogen
847	81	2.9	906	2	T28034	hypothetical prote
848	81	2.9	920	2	F64697	isoleucine-tRNA li
849	81	2.9	964	2	S57379	MSH2 protein - yea
850	81	2.9	1024	2	C64208	hypothetical prote
851	81	2.9	1122	2	A97814	transcription-repa
852	81	2.9	1124	2	F71719	hypothetical prote
853	81	2.9	1126	1	WMFM12	125K protein - alf
854	81	2.9	1253	2	S62544	hypothetical prote
855	81	2.9	1544	2	G96904	DNA segregation AT
856	81	2.9	1678	2	S52588	clathrin heavy cha
857	81	2.9	1986	2	S28353	probable polyketid
858	81	2.9	3084	1	MMMSA	laminin alpha-1 ch
859	80.5	2.9	339	2	B72402	UDP-N-acetylglucos
860	80.5	2.9	345	2	D70564	hypothetical prote
861	80.5	2.9	360	2	G64686	conserved hypothet
862	80.5	2.9	375	2	S63442	probable protein k
863	80.5	2.9	398	2	A37274	glia-derived nexin
864	80.5	2.9	403	2	A71484	probable phosphogl
865	80.5	2.9	423	2	AD2455	hypothetical prote
866	80.5	2.9	430	2	S77279	hypothetical prote
867	80.5	2.9	435	2	A81416	probable integral
868	80.5	2.9	435	2	H71910	probable processin

869	80.5	2.9	439	2	A83363	probable cytochrom
870	80.5	2.9	446	2	H97929	histidine kinase (
871	80.5	2.9	453	2	AF2401	cytochrome P450 [i
872	80.5	2.9	461	2	T47782	hypothetical prote
873	80.5	2.9	488	1	QXASM4	NADH2 dehydrogenas
874	80.5	2.9	491	2	AC1499	transmembrane prot
875	80.5	2.9	492	2	A34272	testosterone 7alph
876	80.5	2.9	499	2	S53637	protein kinase clk
877	80.5	2.9	562	2	T29858	hypothetical prote
878	80.5	2.9	583	2	G83375	probable glycosyl
879	80.5	2.9	595	2	E82934	hypothetical prote
880	80.5	2.9	642	2	S64348	hypothetical prote
881	80.5	2.9	652	2	H86221	hypothetical prote
882	80.5	2.9	698	2	T12629	NADH2 dehydrogenas
883	80.5	2.9	698	2	T12625	NADH2 dehydrogenas
884	80.5	2.9	702	2	T12624	NADH2 dehydrogenas
885	80.5	2.9	719	2	T13793	NADH2 dehydrogenas
886	80.5	2.9	741	2	T13764	NADH2 dehydrogenas
887	80.5	2.9	741	2	T13663	NADH2 dehydrogenas
888	80.5	2.9	744	2	T12714	NADH2 dehydrogenas
889	80.5	2.9	826	2	T33796	hypothetical prote
890	80.5	2.9	984	2	D70461	preprotein translo
891	80.5	2.9	1025	2	I59331	thyrotropin-releas
892	80.5	2.9	1032	2	S12153	pol polyprotein -
893	80.5	2.9	1042	2	H75112	molybdenum cofacto
894	80.5	2.9	1301	2	T07321	DNA-directed RNA p
895	80.5	2.9	1568	2	T41013	hypothetical prote
896	80	2.9	217	2	E97310	uncharacterized co
897	80	2.9	285	2	D69632	transcription anti
898	80	2.9	318	2	D71501	hypothetical prote
899	80	2.9	324	2	E91186	probable transcrip
900	80	2.9	324	2	D86033	probable transcrip
901	80	2.9	333	2	S77222	hypothetical prote
902	80	2.9	366	2	C81336	RodA protein homol
903	80	2.9	394	2	B70411	fimbrial assembly
904	80	2.9	397	2	I48717	proteinase inhibit
905	80	2.9	404	2	H95937	hypothetical prote
906	80	2.9	404	2	T44600	hypothetical prote
907	80	2.9	413	2	S52018	translation initia
908	80	2.9	420	1	S34379	glycine hydroxymet
909	80	2.9	426	2	A40440	endothelin 1 and 2
910	80	2.9	466	2	H84971	asparagine-tRNA li
911	80	2.9	486	2	E96757	protein glycosyl t
912	80	2.9	494	2	JC5320	cytochrome P450 mo
913	80	2.9	510	1	A56926	activin receptor I
914	80	2.9	545	2	T40207	hypothetical prote
915	80	2.9	567	2	E72156	C6R protein - vari
916	80	2.9	567	2	I36841	E6R protein - vari
917	80	2.9	567	2	T28485	hypothetical prote
918	80	2.9	610	1	DCZMP	pyruvate decarboxy
919	80	2.9	640	2	F71527	probable transketo
920	80	2.9	663	2	T41963	hypothetical prote
921	80	2.9	685	2	AF0850	hypothetical prote
922	80	2.9	686	2	T12607	NADH2 dehydrogenas
923	80	2.9	686	2	T12128	NADH2 dehydrogenas
924	80	2.9	697	2	T13670	NADH2 dehydrogenas
925	80	2.9	698	2	T12713	NADH2 dehydrogenas

926	80	2.9	698	2	T12567	NADH2 dehydrogenas
927	80	2.9	700	2	T13661	NADH2 dehydrogenas
928	80	2.9	741	2	T13705	NADH2 dehydrogenas
929	80	2.9	744	2	T13399	NADH2 dehydrogenas
930	80	2.9	760	2	T34414	hypothetical prote
931	80	2.9	775	2	E70320	polyribonucleotide
932	80	2.9	789	2	T09672	ent-kaurene syntha
933	80	2.9	826	1	T02753	S-receptor kinase
934	80	2.9	906	2	B96901	uncharacterized co
935	80	2.9	920	2	T10052	aminopeptidase (EC
936	80	2.9	950	2	T09076	hypothetical prote
937	80	2.9	1183	2	F90559	conserved hypothet
938	80	2.9	1356	2	S51389	ROM2 protein - yea
939	80	2.9	1620	2	E83261	conserved hypothet
940	80	2.9	2108	2	S28417	CDC39 protein - ye
941	80	2.9	2178	2	S55805	alpha-toxin - Clos
942	80	2.9	3744	2	S46715	hypothetical prote
943	80	2.9	5232	2	A45086	HC-toxin synthetas
944	80	2.9	7962	2	I38346	elastic titin - hu
945	79.5	2.9	271	2	G84030	hemA concentration
946	79.5	2.9	292	2	S57107	hypothetical prote
947	79.5	2.9	295	2	F83356	hypothetical prote
948	79.5	2.9	328	2	H64554	heat shock protein
949	79.5	2.9	336	2	E96814	hypothetical prote
950	79.5	2.9	351	2	B86261	UDPglucose 4-epime
951	79.5	2.9	369	2	H82357	tRNA (uracil-5-)-m
952	79.5	2.9	389	2	B71865	cyclopropane-fatty
953	79.5	2.9	407	2	D71862	probable zinc-meta
954	79.5	2.9	423	2	I64063	histidine-tRNA lig
955	79.5	2.9	449	2	JU0154	tubulin alpha chai
956	79.5	2.9	471	1	KIRTFB	6-phosphofructo-2-
957	79.5	2.9	480	2	G71664	UDP-n-acetylmuramo
958	79.5	2.9	511	2	T39884	hypothetical prote
959	79.5	2.9	512	2	F71915	hypothetical prote
960	79.5	2.9	525	2	S67289	alcohol O-acetyltr
961	79.5	2.9	526	2	A75581	flavin monoamine o
962	79.5	2.9	542	1	T02074	4-coumarate-CoA li
963	79.5	2.9	557	2	A99702	conserved hypothet
964	79.5	2.9	562	2	S01312	alpha-amylase (EC
965	79.5	2.9	603	2	T48154	pyruvate decarboxy
966	79.5	2.9	608	2	D72306	hypothetical prote
967	79.5	2.9	625	2	H70330	hypothetical prote
968	79.5	2.9	631	2	T38167	electron transfer
969	79.5	2.9	642	2	A75062	hypothetical prote
970	79.5	2.9	739	2	T13770	NADH2 dehydrogenas
971	79.5	2.9	741	2	T12701	NADH2 dehydrogenas
972	79.5	2.9	741	2	T12702	NADH2 dehydrogenas
973	79.5	2.9	767	2	A46361	P element homolog
974	79.5	2.9	860	2	T37768	probable vacuolar
975	79.5	2.9	867	2	AC2140	ferrichrome-iron r
976	79.5	2.9	880	2	T21538	hypothetical prote
977	79.5	2.9	909	1	A54809	disease resistance
978	79.5	2.9	956	2	B83200	probable phosphotr
979	79.5	2.9	973	2	A75135	probable DEAH ATP-
980	79.5	2.9	1021	2	E64576	hypothetical prote
981	79.5	2.9	1026	2	T03179	probable DNA-direc
982	79.5	2.9	1035	2	C87373	TonB-dependent rec

983	79.5	2.9	1061	2	C88690	protein F41H10.4 [
984	79.5	2.9	1146	2	B70376	reverse gyrase - A
985	79.5	2.9	1152	2	T21853	hypothetical prote
986	79.5	2.9	1274	2	T02636	D1 protein homolog
987	79.5	2.9	1367	2	T21913	hypothetical prote
988	79.5	2.9	2342	2	T18200	fatty-acid synthas
989	79.5	2.9	4131	2	T21085	hypothetical prote
990	79.5	2.9	4450	2	JX0340	gramicidin S synth
991	79	2.9	224	2	F81744	conserved hypothet
992	79	2.9	238	1	B64313	probable 3-isoprop
993	79	2.9	252	2	A99976	cyclase-like prote
994	79	2.9	262	2	D89968	hypothetical prote
995	79	2.9	330	2	G75007	lps biosynthesis r
996	79	2.9	331	2	E86638	hypothetical prote
997	79	2.9	337	2	S28045	cinnamyl-alcohol d
998	79	2.9	345	2	B42604	ORF2 complementary
999	79	2.9	409	2	S73724	ATP-dependent RNA
1000	79	2.9	410	2	G64637	D-amino acid dehyd
1001	79	2.9	413	2	S22578	translation initia
1002	79	2.9	413	2	S52023	translation initia
1003	79	2.9	413	2	S52019	translation initia
1004	79	2.9	413	2	S55898	translation initia
1005	79	2.9	422	2	C75631	probable Na ⁺ /H ⁺ an
1006	79	2.9	437	2	G91067	hypothetical prote
1007	79	2.9	441	2	H85911	hypothetical prote
1008	79	2.9	452	2	T39693	hypothetical prote
1009	79	2.9	460	2	T16307	hypothetical prote
1010	79	2.9	466	2	S29247	argininosuccinate
1011	79	2.9	470	2	S57902	peptidase V - Lact
1012	79	2.9	477	2	D90112	hypothetical prote
1013	79	2.9	501	2	C49930	hypothetical prote
1014	79	2.9	531	2	H81137	funZ protein NMB09
1015	79	2.9	540	2	G96716	hypothetical prote
1016	79	2.9	556	2	C72204	alpha-amylase - Th
1017	79	2.9	557	2	H95237	transcription regu
1018	79	2.9	559	2	E90288	restriction endonu
1019	79	2.9	567	2	T30799	hypothetical prote
1020	79	2.9	567	2	E35928	hypothetical prote
1021	79	2.9	567	2	A42509	E6R protein - vacc
1022	79	2.9	583	2	A82430	nitrate/nitrite se
1023	79	2.9	607	2	T05315	pyruvate decarboxy
1024	79	2.9	635	2	A71620	hypothetical prote
1025	79	2.9	676	2	B72071	ribonuclease famil
1026	79	2.9	676	2	D86553	ribonuclease famil
1027	79	2.9	679	2	S64258	hypothetical prote
1028	79	2.9	687	2	S43250	thimet oligopeptid
1029	79	2.9	688	2	T13672	NADH2 dehydrogenas
1030	79	2.9	689	2	T13681	NADH2 dehydrogenas
1031	79	2.9	690	2	T13786	NADH2 dehydrogenas
1032	79	2.9	694	2	T13572	NADH2 dehydrogenas
1033	79	2.9	698	2	T13492	NADH2 dehydrogenas
1034	79	2.9	698	2	T12568	NADH2 dehydrogenas
1035	79	2.9	698	2	T13769	NADH2 dehydrogenas
1036	79	2.9	702	2	T12141	NADH2 dehydrogenas
1037	79	2.9	736	2	T12214	NADH2 dehydrogenas
1038	79	2.9	758	2	D71072	hypothetical prote
1039	79	2.9	937	2	C97168	glycosyltransferas

1040	79	2.9	1002	2	I56963	transposase - Esch
1041	79	2.9	1036	2	E96682	hypothetical prote
1042	79	2.9	1061	1	DJAD12	DNA-directed DNA p
1043	79	2.9	1261	2	S75130	sensory transducti
1044	79	2.9	1441	2	T39636	probable cleavage
1045	79	2.9	1549	2	T13940	ankyrin - fruit fl
1046	79	2.9	1616	2	G70668	polyketide synthas
1047	78.5	2.8	246	2	T14772	hypothetical prote
1048	78.5	2.8	254	2	A56447	CMP-2-keto-3-deoxy
1049	78.5	2.8	299	2	AE0461	probable membrane
1050	78.5	2.8	315	2	S58689	hypothetical prote
1051	78.5	2.8	328	2	H71954	probable lipid A b
1052	78.5	2.8	406	2	D71905	hypothetical prote
1053	78.5	2.8	457	1	G70116	histidine-tRNA lig
1054	78.5	2.8	463	2	AI1744	B. subtilis YunD p
1055	78.5	2.8	467	2	A48916	sodium phosphate t
1056	78.5	2.8	489	2	T13026	hypothetical prote
1057	78.5	2.8	506	2	H83396	probable aldehyde
1058	78.5	2.8	506	2	F83142	probable aldehyde
1059	78.5	2.8	524	2	F84511	hypothetical prote
1060	78.5	2.8	562	1	QQBEH5	phosphotransferase
1061	78.5	2.8	579	2	AE1855	hypothetical prote
1062	78.5	2.8	585	2	T28884	hypothetical prote
1063	78.5	2.8	610	2	C96732	hypothetical prote
1064	78.5	2.8	735	2	AE1858	anthranilate synth
1065	78.5	2.8	740	2	T12223	NADH2 dehydrogenas
1066	78.5	2.8	741	2	T12605	NADH2 dehydrogenas
1067	78.5	2.8	741	2	T12614	NADH2 dehydrogenas
1068	78.5	2.8	744	2	T12705	NADH2 dehydrogenas
1069	78.5	2.8	744	2	T13502	NADH2 dehydrogenas
1070	78.5	2.8	744	2	T13570	NADH2 dehydrogenas
1071	78.5	2.8	771	2	T01315	hypothetical prote
1072	78.5	2.8	823	2	G83905	hypothetical prote
1073	78.5	2.8	889	2	T29590	hypothetical prote
1074	78.5	2.8	937	2	B86210	protein F22G5.6 [i
1075	78.5	2.8	943	2	F69543	ATP-dependent RNA
1076	78.5	2.8	1030	2	S73944	hypothetical prote
1077	78.5	2.8	1035	1	GNFFG1	HIV-1 retropepsin
1078	78.5	2.8	1039	2	S76747	hypothetical prote
1079	78.5	2.8	1042	2	G64514	type I restriction
1080	78.5	2.8	1084	2	S23319	hypothetical prote
1081	78.5	2.8	1120	2	H88449	protein F54D8.1 [i
1082	78.5	2.8	1131	2	T16217	hypothetical prote
1083	78.5	2.8	1199	2	T18348	probable pol polyp
1084	78.5	2.8	1572	2	S45251	SNF2alpha protein
1085	78.5	2.8	1586	2	S39580	HBRM protein - hum
1086	78.5	2.8	1663	1	C3RT	complement C3 prec
1087	78.5	2.8	1799	1	S44920	ZK688.5 protein -
1088	78.5	2.8	2166	2	G70163	hypothetical prote
1089	78	2.8	146	2	G75215	methylmalonyl-coa
1090	78	2.8	208	2	A38202	GTP-binding protei
1091	78	2.8	230	2	T15381	hypothetical prote
1092	78	2.8	252	2	T03140	uracil-DNA glucosi
1093	78	2.8	256	2	AI1204	molybdate ABC tran
1094	78	2.8	297	2	AI1135	transcription regu
1095	78	2.8	319	2	H90321	transposase ISC123
1096	78	2.8	365	2	A30891	regulatory protein

1097	78	2.8	366	2	E72355	hypothetical prote
1098	78	2.8	374	2	B72285	hypothetical prote
1099	78	2.8	394	2	A64713	folylpolyglutamate
1100	78	2.8	398	2	B70752	hypothetical prote
1101	78	2.8	403	2	G82831	queueine tRNA-ribos
1102	78	2.8	415	2	A54126	endothelin recepto
1103	78	2.8	422	2	F64581	UDP-N-acetylmuramo
1104	78	2.8	424	2	I39506	citrate (si)-synth
1105	78	2.8	431	2	H81981	probable tyrosine-
1106	78	2.8	431	2	A81037	tyrosyl-tRNA synth
1107	78	2.8	467	2	T04540	adenylosuccinate l
1108	78	2.8	474	2	E95043	hypothetical prote
1109	78	2.8	474	2	G97913	phosphogluconate d
1110	78	2.8	500	2	JC4709	steroid 11beta-mon
1111	78	2.8	503	2	A29815	cytochrome P450 3A
1112	78	2.8	552	2	S69032	hypothetical prote
1113	78	2.8	554	2	S75969	hypothetical prote
1114	78	2.8	558	2	F81967	probable inner mem
1115	78	2.8	596	2	AD1876	hypothetical prote
1116	78	2.8	606	2	E90536	hypothetical prote
1117	78	2.8	607	2	T39823	hypothetical prote
1118	78	2.8	612	2	B81246	glutamine-fructose
1119	78	2.8	633	2	T52506	hypothetical prote
1120	78	2.8	691	2	T13567	NADH2 dehydrogenas
1121	78	2.8	701	2	T13568	NADH2 dehydrogenas
1122	78	2.8	786	2	S71091	acetyl-CoA carboxy
1123	78	2.8	805	2	T03896	hypothetical prote
1124	78	2.8	808	2	T49233	sucrose synthase-l
1125	78	2.8	833	2	T28385	ORF MSV224 probabl
1126	78	2.8	855	2	T47534	hypothetical prote
1127	78	2.8	857	2	T37459	ribonucleotide red
1128	78	2.8	865	2	T30998	hypothetical prote
1129	78	2.8	870	2	B71698	hypothetical prote
1130	78	2.8	876	2	A89944	alanyl-tRNA synthe
1131	78	2.8	877	2	H71647	alanine-tRNA ligas
1132	78	2.8	878	2	G97865	alanine-tRNA ligas
1133	78	2.8	887	2	S70642	ubiquitin ligase N
1134	78	2.8	901	1	RGECMT	regulatory protein
1135	78	2.8	901	2	D91161	positive regulator
1136	78	2.8	901	2	D86007	positive regulator
1137	78	2.8	913	2	D82885	multiple banded an
1138	78	2.8	920	2	F71823	isoleucine-tRNA li
1139	78	2.8	987	2	I48953	eph-related recept
1140	78	2.8	993	2	F97717	hypothetical prote
1141	78	2.8	1091	2	T30256	calcium channel al
1142	78	2.8	1122	1	NCECXV	exodeoxyribonuclea
1143	78	2.8	1122	2	G91088	DNA helicase RecC
1144	78	2.8	1122	2	A85934	DNA helicase RecC
1145	78	2.8	1138	2	S64484	phosphatidylserine
1146	78	2.8	1237	2	S64385	probable membrane
1147	78	2.8	1680	2	T41628	probable transcrip
1148	78	2.8	1706	2	I84499	zinc finger protei
1149	78	2.8	1928	2	JS0610	beta-galactosidase
1150	78	2.8	2049	2	T29227	hypothetical prote
1151	78	2.8	2182	2	T28634	variant-specific s
1152	78	2.8	2242	2	A57541	pyrimidine synthes
1153	78	2.8	2535	2	T02646	hypothetical prote

1154	78	2.8	2555	2	C69681	peptide synthetase
1155	78	2.8	2787	2	S45416	TEL1 protein - yea
1156	77.5	2.8	235	2	H81451	ubiquinone/menaqui
1157	77.5	2.8	258	2	T41212	hypothetical wtf6
1158	77.5	2.8	260	2	F97761	hypothetical prote
1159	77.5	2.8	263	2	H71495	probable chltr pla
1160	77.5	2.8	269	2	G90261	serine/threonine p
1161	77.5	2.8	317	1	C70356	conserved hypothet
1162	77.5	2.8	320	1	H69308	conserved hypothet
1163	77.5	2.8	325	2	B89909	GMP reductase (EC
1164	77.5	2.8	342	2	T25143	hypothetical prote
1165	77.5	2.8	346	2	AH1603	conserved hypothet
1166	77.5	2.8	413	2	S60244	translation initia
1167	77.5	2.8	448	2	T28089	hypothetical prote
1168	77.5	2.8	450	2	A56622	tubulin alpha chai
1169	77.5	2.8	497	2	F90471	hypothetical prote
1170	77.5	2.8	517	2	S36712	FUN26 protein - ye
1171	77.5	2.8	540	2	T32230	hypothetical prote
1172	77.5	2.8	552	2	AD1824	periplasmic oligop
1173	77.5	2.8	566	2	C97019	probable membrane
1174	77.5	2.8	622	1	H69480	carbon-monoxide de
1175	77.5	2.8	636	2	JC4960	DNA topoisomerase
1176	77.5	2.8	659	2	G95201	serine/threonine p
1177	77.5	2.8	659	2	G98068	eukaryotic-type se
1178	77.5	2.8	706	2	T12748	NADH2 dehydrogenas
1179	77.5	2.8	736	2	T12716	NADH2 dehydrogenas
1180	77.5	2.8	741	2	T13403	NADH2 dehydrogenas
1181	77.5	2.8	744	2	T13048	NADH2 dehydrogenas
1182	77.5	2.8	746	2	T29661	hypothetical prote
1183	77.5	2.8	784	2	T26585	hypothetical prote
1184	77.5	2.8	860	2	A96717	unknown protein, 4
1185	77.5	2.8	901	2	F89910	aconitate hydratase
1186	77.5	2.8	929	2	S75098	hypothetical prote
1187	77.5	2.8	967	2	D96573	protein F12M16.21
1188	77.5	2.8	978	2	H81311	transcription-repa
1189	77.5	2.8	994	2	B82843	valyl-tRNA synthet
1190	77.5	2.8	1052	2	T00067	hypothetical prote
1191	77.5	2.8	1178	2	S54073	probable membrane
1192	77.5	2.8	1186	2	H88869	protein unc-31 [im
1193	77.5	2.8	1212	2	A96971	cobalamine-depende
1194	77.5	2.8	1242	2	T39453	probable mrna stab
1195	77.5	2.8	2514	2	T37320	ataxia telangiecta
1196	77.5	2.8	2619	2	T24588	hypothetical prote
1197	77.5	2.8	2819	2	A90551	conserved hypothet
1198	77.5	2.8	3635	2	T10053	laminin alpha 5 ch
1199	77.5	2.8	4767	2	T31345	hypothetical prote
1200	77	2.8	295	2	F70936	hypothetical prote
1201	77	2.8	297	2	AE2805	permease [imported
1202	77	2.8	319	2	D90344	transposase ISC123
1203	77	2.8	319	2	D90350	transposase ISC123
1204	77	2.8	319	2	E90466	transposase ISC123
1205	77	2.8	319	2	G90428	transposase ISC123
1206	77	2.8	324	2	S47806	probable transcrip
1207	77	2.8	376	2	AE1786	cell division prot
1208	77	2.8	387	2	T31748	hypothetical prote
1209	77	2.8	393	2	AD2219	hypothetical prote
1210	77	2.8	407	2	F64567	zinc metalloprotei

1211	77	2.8	412	2	JC1453	translation initia
1212	77	2.8	420	2	I49708	GTP-binding protei
1213	77	2.8	429	2	T29711	hypothetical prote
1214	77	2.8	449	2	JC6560	UDP-N-acetylmuramo
1215	77	2.8	487	2	AE0310	NADH2 dehydrogenas
1216	77	2.8	503	2	S59698	HST1 protein - yea
1217	77	2.8	513	2	T38044	hypothetical prote
1218	77	2.8	534	2	T23425	hypothetical prote
1219	77	2.8	545	2	D75208	sugar abc transpor
1220	77	2.8	601	2	T37979	hypothetical prote
1221	77	2.8	608	2	G82137	pvcA protein VC194
1222	77	2.8	612	2	JC7101	carnitine O-octano
1223	77	2.8	635	2	S36718	phosphoprotein pho
1224	77	2.8	665	2	S70706	probable protein k
1225	77	2.8	685	2	T19968	hypothetical prote
1226	77	2.8	687	2	T12126	NADH2 dehydrogenas
1227	77	2.8	692	2	T52120	acyl-CoA oxidase (
1228	77	2.8	698	2	T12161	NADH2 dehydrogenas
1229	77	2.8	701	2	T13587	NADH2 dehydrogenas
1230	77	2.8	702	2	T13655	NADH2 dehydrogenas
1231	77	2.8	712	2	T16338	hypothetical prote
1232	77	2.8	713	2	H83684	hypothetical prote
1233	77	2.8	734	2	T13785	NADH2 dehydrogenas
1234	77	2.8	755	2	T48553	subtilisin-like pr
1235	77	2.8	756	2	H75016	hypothetical prote
1236	77	2.8	798	2	AE1263	exodeoxyribonuclea
1237	77	2.8	805	2	C88037	protein K02E7.3 [i
1238	77	2.8	829	1	A47373	protein-tyrosine-p
1239	77	2.8	838	2	T08423	Axin homolog Axil
1240	77	2.8	870	2	B82732	glycerol-3-phospha
1241	77	2.8	891	2	B48642	aconitate hydratase
1242	77	2.8	903	2	C83044	Mg(2+) transport A
1243	77	2.8	932	2	T32417	hypothetical prote
1244	77	2.8	978	2	T00336	hypothetical prote
1245	77	2.8	995	2	AE1773	formate dehydrogen
1246	77	2.8	1035	1	GNLJGG	HIV-1 retropepsin
1247	77	2.8	1086	2	A88855	protein M18.5 [imp
1248	77	2.8	1134	2	T23798	hypothetical prote
1249	77	2.8	1188	2	G72734	hypothetical prote
1250	77	2.8	1217	2	D88996	protein C17B7.7 [i
1251	77	2.8	1441	1	GNVUSV	M polyprotein prec
1252	77	2.8	1442	2	S72441	protein-tyrosine-p
1253	77	2.8	1751	2	A45604	major blood-stage
1254	77	2.8	2027	2	S60123	hypothetical prote
1255	77	2.8	2056	2	G88564	protein R10E11.1 [
1256	77	2.8	2109	1	ZLVNNJ	genome polyprotein
1257	77	2.8	2210	1	RRXPLC	genome polyprotein
1258	77	2.8	2470	2	S57085	1-phosphatidylinos
1259	77	2.8	4572	2	S57908	hypothetical 527K
1260	76.5	2.8	183	1	D64430	probable transcrip
1261	76.5	2.8	251	2	C70238	conserved hypothet
1262	76.5	2.8	257	2	AH1561	molybdate ABC tran
1263	76.5	2.8	334	2	E95869	probable smc22-r p
1264	76.5	2.8	338	2	T06336	proline-rich prote
1265	76.5	2.8	381	2	H83985	alpha-D-mannose-al
1266	76.5	2.8	389	2	S75454	hypothetical prote
1267	76.5	2.8	389	2	H64571	cyclopropane-fatty

1268	76.5	2.8	390	2	E69272	conserved hypothet
1269	76.5	2.8	398	2	G81451	hypothetical prote
1270	76.5	2.8	406	2	G64608	hypothetical prote
1271	76.5	2.8	409	2	C95041	hypothetical prote
1272	76.5	2.8	411	2	T47406	hypothetical prote
1273	76.5	2.8	417	2	A64380	phosphoglycerate k
1274	76.5	2.8	421	2	AE2473	hypothetical prote
1275	76.5	2.8	426	2	JH0690	bone morphogenetic
1276	76.5	2.8	462	2	AH1130	glutamate decarbox
1277	76.5	2.8	465	2	I39473	Na+-dependent phos
1278	76.5	2.8	524	1	O4MSM1	aryl hydrocarbon (
1279	76.5	2.8	525	2	S69991	alcohol O-acetyltr
1280	76.5	2.8	533	2	T07970	aromatic-L-amino-a
1281	76.5	2.8	537	2	C64432	hypothetical prote
1282	76.5	2.8	562	2	E64412	hypothetical prote
1283	76.5	2.8	567	2	T08405	hypothetical prote
1284	76.5	2.8	569	2	A45624	trophozoite cystei
1285	76.5	2.8	569	2	T19128	hypothetical prote
1286	76.5	2.8	595	2	AI0042	thiol,disulfide in
1287	76.5	2.8	600	2	C69371	conserved hypothet
1288	76.5	2.8	619	2	A60646	transforming prote
1289	76.5	2.8	636	2	A45949	merozoite surface
1290	76.5	2.8	666	2	T13584	NADH2 dehydrogenas
1291	76.5	2.8	676	2	AF1153	transcription anti
1292	76.5	2.8	677	2	T18231	transketolase I -
1293	76.5	2.8	682	2	D90946	hypothetical prote
1294	76.5	2.8	682	2	H85794	hypothetical prote
1295	76.5	2.8	682	2	A41798	carboxy-terminal p
1296	76.5	2.8	683	2	T12127	NADH2 dehydrogenas
1297	76.5	2.8	699	2	T13730	NADH2 dehydrogenas
1298	76.5	2.8	704	2	T13729	NADH2 dehydrogenas
1299	76.5	2.8	726	2	T31287	hypothetical prote
1300	76.5	2.8	746	2	T13698	NADH2 dehydrogenas
1301	76.5	2.8	746	2	T13678	NADH2 dehydrogenas
1302	76.5	2.8	753	2	C96668	unknown protein F1
1303	76.5	2.8	753	2	T32844	hypothetical prote
1304	76.5	2.8	756	2	A88679	protein H06H21.10
1305	76.5	2.8	885	1	A55453	nucleotide diphosp
1306	76.5	2.8	889	2	C72565	probable valyl-tRN
1307	76.5	2.8	899	2	F84477	probable retroelem
1308	76.5	2.8	900	2	T14277	myosin-like protei
1309	76.5	2.8	904	2	T46170	disease resistance
1310	76.5	2.8	962	2	S67385	hypothetical prote
1311	76.5	2.8	990	2	S42586	transposase - Rhiz
1312	76.5	2.8	1018	2	E83099	probable RND efflu
1313	76.5	2.8	1054	2	G82934	hypothetical prote
1314	76.5	2.8	1125	1	JH0771	protein-tyrosine k
1315	76.5	2.8	1134	2	T04890	hypothetical prote
1316	76.5	2.8	1212	2	A84500	probable retroelem
1317	76.5	2.8	1217	2	H89863	hypothetical prote
1318	76.5	2.8	1333	2	S30356	CDC25 protein homo
1319	76.5	2.8	1384	2	S78132	DNA-directed RNA p
1320	76.5	2.8	1434	2	C90109	DNA-directed RNA p
1321	76.5	2.8	1447	2	S63669	UDPglucose-glycopr
1322	76.5	2.8	1497	2	S72250	sex-determining tr
1323	76.5	2.8	1613	2	S39059	protein BRG1 - hum
1324	76.5	2.8	1726	2	A39401	merozoite surface

1325	76.5	2.8	1827	2	A35694	cutl protein - fis
1326	76.5	2.8	2025	2	JC5020	tetratricopeptide
1327	76.5	2.8	2216	2	S78398	hypothetical prote
1328	76	2.7	147	2	D71452	probable methylmal
1329	76	2.7	279	2	T03830	probable myb facto
1330	76	2.7	294	2	G95120	conserved hypothet
1331	76	2.7	301	2	AB1679	dehydrogenases and
1332	76	2.7	319	2	D90342	transposase ISC123
1333	76	2.7	331	2	B70336	heterodisulfide re
1334	76	2.7	401	2	T25031	hypothetical prote
1335	76	2.7	402	2	T43603	transcription repr
1336	76	2.7	409	2	T47754	leucine zipper-con
1337	76	2.7	416	2	S77027	hypothetical prote
1338	76	2.7	445	2	AE1590	hypothetical prote
1339	76	2.7	450	2	F69371	bile acid-inducibl
1340	76	2.7	452	2	S41717	aspartic hemoglobi
1341	76	2.7	454	2	PC4237	trans-cinnamate 4-
1342	76	2.7	500	2	JX0252	aldosterone syntha
1343	76	2.7	502	2	G87433	conserved hypothet
1344	76	2.7	510	2	A35342	steroid 11beta-mon
1345	76	2.7	519	2	C90085	hypothetical prote
1346	76	2.7	527	2	G71557	probable glucanotr
1347	76	2.7	537	2	T38015	hypothetical prote
1348	76	2.7	545	2	H86322	calcium-dependent
1349	76	2.7	550	2	D88099	protein F18A12.5 [
1350	76	2.7	593	2	A72221	conserved hypothet
1351	76	2.7	646	2	T38212	hypothetical prote
1352	76	2.7	658	2	A64584	hypothetical prote
1353	76	2.7	666	2	T44207	DNA-packaging prot
1354	76	2.7	672	2	A72076	hypothetical prote
1355	76	2.7	672	2	B86548	hypothetical prote
1356	76	2.7	675	2	A35743	creatine kinase (E
1357	76	2.7	682	2	T12294	NADH2 dehydrogenas
1358	76	2.7	682	2	AE0728	tail-specific prot
1359	76	2.7	698	2	H71535	hypothetical prote
1360	76	2.7	702	2	T12677	NADH2 dehydrogenas
1361	76	2.7	711	2	G86526	hypothetical prote
1362	76	2.7	711	2	A72098	hypothetical prote
1363	76	2.7	744	2	T13757	NADH2 dehydrogenas
1364	76	2.7	788	2	B84857	hypothetical prote
1365	76	2.7	789	2	S49240	hypothetical prote
1366	76	2.7	791	2	E35216	FPD5 protein - fow
1367	76	2.7	813	2	T40622	translation elonga
1368	76	2.7	815	2	G82417	conserved hypothet
1369	76	2.7	821	2	H71475	probable chltr pho
1370	76	2.7	830	2	S54547	PAM1 protein - yea
1371	76	2.7	867	2	E86815	ClpB protein [impo
1372	76	2.7	882	2	T39789	aminopeptidase - f
1373	76	2.7	891	2	T38195	probable alpha,alp
1374	76	2.7	902	2	AG2989	preprotein translo
1375	76	2.7	907	1	A57429	aldehyde oxidase (
1376	76	2.7	919	2	B98294	preprotein translo
1377	76	2.7	987	2	I48652	mouse developmenta
1378	76	2.7	1013	2	B96544	hypothetical prote
1379	76	2.7	1058	1	GNFF17	retrovirus-related
1380	76	2.7	1083	2	A38919	hypothetical prote
1381	76	2.7	1146	2	E70204	hypothetical prote

1382	76	2.7	1187	2	C84568	hypothetical prote
1383	76	2.7	1195	2	T43735	pyruvate carboxyla
1384	76	2.7	1240	2	T06404	resistance complex
1385	76	2.7	1476	2	JC5143	alpha-macroglobuli
1386	76	2.7	1777	2	T00490	nonstructural prot
1387	76	2.7	2077	2	T44178	large tegument pro
1388	76	2.7	2124	2	T01526	hypothetical prote
1389	76	2.7	3944	2	T19997	hypothetical prote
1390	76	2.7	4725	1	A44357	dynein heavy chain
1391	75.5	2.7	244	2	D64232	glycerophosphoryl
1392	75.5	2.7	246	2	F75453	5,10-methylenetet
1393	75.5	2.7	333	2	T29242	hypothetical prote
1394	75.5	2.7	349	2	S74862	hypothetical prote
1395	75.5	2.7	362	2	C82070	conserved hypothet
1396	75.5	2.7	419	2	AF1274	tyrosyl-tRNA synth
1397	75.5	2.7	431	2	T32694	hypothetical prote
1398	75.5	2.7	450	2	A26488	tubulin alpha-1 ch
1399	75.5	2.7	461	2	E71672	fumarate hydratase
1400	75.5	2.7	474	2	S60902	CDP-ribitol pyroph
1401	75.5	2.7	477	2	T30012	hypothetical prote
1402	75.5	2.7	484	2	E64432	spore coat polysac
1403	75.5	2.7	492	2	T23502	hypothetical prote
1404	75.5	2.7	494	2	T03774	probable histidine
1405	75.5	2.7	494	2	D70579	probable murC prot
1406	75.5	2.7	497	2	G81598	serine hydroxymeth
1407	75.5	2.7	514	2	C70446	hypothetical prote
1408	75.5	2.7	515	2	E86534	ADP/ATP translocas
1409	75.5	2.7	515	2	E72089	ADP, ATP carrier p
1410	75.5	2.7	519	2	E86555	serine hydroxymeth
1411	75.5	2.7	519	2	H72067	glycine hydroxymet
1412	75.5	2.7	519	2	S70581	dihydropyrimidinas
1413	75.5	2.7	526	2	S34945	nitrogenase (EC 1.
1414	75.5	2.7	541	2	G90192	conserved hypothet
1415	75.5	2.7	542	2	T03789	4-coumarate-CoA li
1416	75.5	2.7	548	2	T41092	hypothetical prote
1417	75.5	2.7	548	2	C82698	electron transfer
1418	75.5	2.7	550	2	JC4112	P-methyltransferas
1419	75.5	2.7	562	2	A96773	hypothetical prote
1420	75.5	2.7	570	2	T00579	probable laccase [
1421	75.5	2.7	594	2	T48583	auxin-regulated pr
1422	75.5	2.7	594	2	T04545	protein cs/ch-42,
1423	75.5	2.7	607	1	NUUTB	glucose-6-phosphat
1424	75.5	2.7	609	2	A64432	nodulation factor
1425	75.5	2.7	633	2	G89836	ABC transporter pe
1426	75.5	2.7	640	2	S69546	phosphoenolpyruvat
1427	75.5	2.7	676	2	T37345	NPH-II, helicase -
1428	75.5	2.7	676	2	D42511	I8R protein - vacc
1429	75.5	2.7	676	2	F36843	ATP/GTP-binding pr
1430	75.5	2.7	676	2	T28500	hypothetical prote
1431	75.5	2.7	682	2	D72158	L8R protein - vari
1432	75.5	2.7	699	2	T13772	NADH2 dehydrogenas
1433	75.5	2.7	705	2	T51788	hypothetical prote
1434	75.5	2.7	708	2	A47176	probable transmemb
1435	75.5	2.7	739	2	T13038	NADH2 dehydrogenas
1436	75.5	2.7	740	2	D97180	relA/SpoT protein,
1437	75.5	2.7	742	2	T13495	NADH2 dehydrogenas
1438	75.5	2.7	743	2	T13700	NADH2 dehydrogenas

1439	75.5	2.7	744	2	T13376	NADH2 dehydrogenas
1440	75.5	2.7	751	2	S38101	hypothetical prote
1441	75.5	2.7	756	2	T12697	NADH2 dehydrogenas
1442	75.5	2.7	782	2	D81281	probable nucleotid
1443	75.5	2.7	787	2	S72725	guanosine-3',5'bis
1444	75.5	2.7	838	2	T09054	capsaicin receptor
1445	75.5	2.7	848	2	B84107	hypothetical prote
1446	75.5	2.7	875	2	D81651	conserved hypothet
1447	75.5	2.7	915	1	A55144	autotaxin precurs
1448	75.5	2.7	928	2	T52292	endopeptidase Clp
1449	75.5	2.7	949	2	H97322	DNA/RNA helicase,
1450	75.5	2.7	971	2	A70179	exodeoxyribonuclea
1451	75.5	2.7	975	2	AC2517	hypothetical prote
1452	75.5	2.7	1022	2	I53078	homeotic gene regu
1453	75.5	2.7	1031	2	T06130	hypothetical prote
1454	75.5	2.7	1155	2	H71456	probable pyrolysin
1455	75.5	2.7	1178	2	S44142	VLA-2 protein homo
1456	75.5	2.7	1225	2	T39255	probable C2 domain
1457	75.5	2.7	1285	2	B72420	hypothetical prote
1458	75.5	2.7	1318	1	HIBPD7	internal virion pr
1459	75.5	2.7	1430	2	S50596	hypothetical prote
1460	75.5	2.7	1450	2	A84780	probable ABC trans
1461	75.5	2.7	1605	2	T31435	DNA-directed RNA p
1462	75.5	2.7	1647	2	S45252	SNF2beta protein -
1463	75.5	2.7	1657	2	T25421	hypothetical prote
1464	75.5	2.7	1764	2	S37827	hypothetical prote
1465	75.5	2.7	1874	1	JQ0533	genome polyprotein
1466	75.5	2.7	2022	2	A59256	myosin-IXb [simila
1467	75.5	2.7	2136	2	A05037	hypothetical prote
1468	75.5	2.7	2471	2	T03820	probable histidine
1469	75.5	2.7	2748	2	S57976	nuclear migration
1470	75.5	2.7	8243	2	T31307	type I fatty acid
1471	75	2.7	249	2	E69298	conserved hypothet
1472	75	2.7	263	2	F45734	orf6 3' to hisD -
1473	75	2.7	288	2	G86223	hypothetical prote
1474	75	2.7	295	1	H70031	conserved hypothet
1475	75	2.7	295	2	G85042	hypothetical prote
1476	75	2.7	312	2	D90198	transposase ISC123
1477	75	2.7	314	2	S75872	hypothetical prote
1478	75	2.7	325	2	F91024	NADH dehydrogenase
1479	75	2.7	325	2	G85868	NADH dehydrogenase
1480	75	2.7	325	2	H64999	NADH2 dehydrogenas
1481	75	2.7	327	2	D82090	conserved hypothet
1482	75	2.7	333	2	AG2121	luciferase-alpha c
1483	75	2.7	350	2	AH3043	dehydrogenase Atu3
1484	75	2.7	350	2	D98242	lipopolysaccharide
1485	75	2.7	357	2	C72022	UDP-N-acetylglucos
1486	75	2.7	357	2	F86603	peptidoglycan tran
1487	75	2.7	372	2	I38042	single-stranded DN
1488	75	2.7	376	2	AE1878	phospho-2-dehydro-
1489	75	2.7	391	2	A89870	hypothetical prote
1490	75	2.7	392	1	SYPJCB	naringenin-chalcon
1491	75	2.7	400	1	F69142	probable hexosyltr
1492	75	2.7	404	2	T19445	hypothetical prote
1493	75	2.7	404	2	C64332	hypothetical prote
1494	75	2.7	408	2	D95392	protein [imported
1495	75	2.7	411	2	G97802	tyrosine-tRNA liga

1496	75	2.7	414	2	D70723	probable transfera
1497	75	2.7	416	2	F81337	RNA polymerase sig
1498	75	2.7	419	2	E64526	hypothetical prote
1499	75	2.7	432	2	G97224	ATP-dependent prot
1500	75	2.7	448	2	T43624	beta tubulin, temp

ALIGNMENTS

RESULT 1

JC5423

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) - human

N;Alternate names: UDP-galactose:ceramide galactosyltransferase

C;Species: Homo sapiens (man)

C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 26-Aug-1999

C;Accession: JC5423

R;Kapitonov, D.; Yu, R.K.

Biochem. Biophys. Res. Commun. 232, 449-453, 1997

A;Title: Cloning, characterization, and expression of human ceramide galactosyltransferase cDNA.

A;Reference number: JC5423; MUID:97242209; PMID:9125199

A;Accession: JC5423

A;Molecule type: mRNA

A;Residues: 1-541 <KAP>

A;Cross-references: GB:U62899

A;Experimental source: fetal glioma cell

C;Comment: This enzyme catalyzes the final step of galactosylceramide synthesis.

C;Genetics:

A;Gene: cgt

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase

F;472-492/Domain: hydrophobic #status predicted <HYD>

F;538-540/Region: endoplasmic reticulum retention signal #status atypical

F;78,333,442/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.3%; Score 700; DB 2; Length 541;
Best Local Similarity 32.2%; Pred. No. 8.7e-47;
Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE	70
		: : : : : : : : :	
Db	11	LWSAVGIAKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD-----	61
Qy	71	EKSQVISWLPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL	119
		: : : : : : : : : : :	
Db	62	-----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK	112
Qy	120	QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPI	179
		: : : : : : : : :	
Db	113	NCDMMVGNHAIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA	172
Qy	180	PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCCRQQHM-----QSTFD	222
		: : : : : : :	
Db	173	PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSFLVLPKYERIMQKYNLLPEKSMYD	232
Qy	223	NTIKEHFTEGSRPVLSHLLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQD	282

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      | :  : || : : | | : | | | | | | | : : | | | : | : |
Db      233 -----LVHGSSLWMLCTDVALEFPRPTLPNVVYVGGILTKPASPLPED 275
Qy      283 LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHL 342
      | : : : : | | | | : | : | : : | | | | | : | | : |
Db      276 LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFs---GPKPKNL 331
Qy      343 AANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVE 402
      | | : : | | | : | | | : | | | | | | : | | | : | | | : |
Db      332 GNNTKLIWLPQNDLLGHSHKIAFVSHGGLNSIFETMYHGVPPVVGIPVFGDHYDTMTRVQ 391
Qy      403 AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || | : : : | : : | : : : | : | | : | | : | | : | | : :
Db      392 AKGMGILLEWKT VTEKELYEALVKVINNP SYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI 451
Qy      463 LQTGGATHLKPYVFQQPWHEQYLFQDV-FVFLGLTL 497
      : : | | | : | | : : : | : | | | | |
Db      452 IRHNGAHLRAAVHQISFCQYFLLDIAFVLLLGAAL 487

```

RESULT 2

A48801

2-hydroxyacylsphingosine 1-beta-galactosyltransferase (EC 2.4.1.45) precursor - rat

N;Alternate names: UDPgalactose-ceramide galactosyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A48801; I56576; S63480

R;Schulte, S.; Stoffel, W.

Proc. Natl. Acad. Sci. U.S.A. 90, 10265-10269, 1993

A;Title: Ceramide UDPgalactosyltransferase from myelinating rat brain: purification, cloning, and expression.

A;Reference number: A48801; MUID:94052143; PMID:7694285

A;Accession: A48801

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 1-541 <SCH>

A;Cross-references: UNIPROT:Q09426; GB:L21698; NID:g437665; PIDN:AAA16108.1; PID:g437666

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIN:139520, NCBIP:139522)

R;Stahl, N.; Jurevics, H.; Morell, P.; Suzuki, K.; Popko, B.

J. Neurosci. Res. 38, 234-242, 1994

A;Title: Isolation, characterization, and expression of cDNA clones that encode rat UDP-galactose:ceramide galactosyltransferase.

A;Reference number: I56576; MUID:94358923; PMID:7521399

A;Accession: I56576

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-541 <RES>

A;Cross-references: EMBL:U07683; NID:g464025; PIDN:AAA50212.1; PID:g464026

R;Schulte, S.; Stoffel, W.

Eur. J. Biochem. 233, 947-953, 1995

A;Title: UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter: copurification, separation and characterization of the two glycoproteins.

A;Reference number: S63480; MUID:96085162; PMID:8521863

A;Accession: S63480
 A;Molecule type: protein
 A;Residues: 21-28,'A',30-31,'Q',33-39;73-77,'X',79-87;155-166,'Q',168-173;315-322;330-331,'EX',334-338,'Q',340-353;416-423;510-515 <SUL>
 A;Experimental source: brain
 C;Function:
 A;Description: transfers galactose from UDP-galactose to ceramide
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-541/Product: 2-hydroxyacylsphingosine 1-beta-galactosyltransferase #status experimental <MAT>
 F;78,333/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 24.7%; Score 684; DB 2; Length 541;
 Best Local Similarity 32.2%; Pred. No. 1.6e-45;
 Matches 165; Conservative 94; Mismatches 184; Indels 70; Gaps 12;

```

Qy      13  LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE 70
      |  | :: |||: : : || : :: | : ||: | :: |
Db      11  LWSAVGIARAAKIIIVPPIMFESHLYIFKTLASALHERGHHTVFLLSEGRD----- 61

Qy      71  EKSQVISWLAPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL 119
      : | : | : : | | ||: : || |::|::
Db      62  -----IDPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAVELVDILDHYTK 112

Qy     120  QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSGSLEFGLPI 179
      | : : :: || | ||::|: | | ||: || : : | | |
Db     113  NCDMMVGNQALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA 172

Qy     180  PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCRRQQH-----MQSTFD 222
      ||: || | |||| | : | | : || ||: : | | : | : |
Db     173  PLAYVPEFNSLLTDRMNFLERMKNTGVYLISRMGVSFVLVPKYERIMQKYNLLPAKSMYD 232

Qy     223  NTIKEHFTEGSRPVLSHLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQD 282
      | : : || : : | | : | || || | |||:: || | : | : |
Db     233  -----LVHGSSLWMLCTDVALEFP RPRTLPNVVYVG GILTKPASPLPED 275

Qy     283  LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHL 342
      | : :: : ||||: | : | : : | :: | || |||: : | : |
Db     276  LQRWVDGAQEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFSGT---KPKNL 331

Qy     343  AANVKIVDWLPQSDLLAHPsirLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVE 402
      | |::: |||: || | : || |:: || | : |||: ||||| | : | | :
Db     332  GNNTKLIEWLPQNDLLGHSNIRAFLSHGGLNSIFETMYHGVPPVVGIPFGDHYDTMTRVQ 391

Qy     403  AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV 462
      || | : :: : | : :: : : | : | | : | | | ||::
Db     392  AKGMGILLEWNTVTEGELYDALVKVINNPYRQRAQKLSEIHKDQPGHPVNRRTTYWIDYI 451

Qy     463  LQTGGATHLKPYVFQQPWHEQYLFQDV-FVFLLG 494
      | : || ||: | | : : : | : || || |
Db     452  LRHDGAHHLRSVHQISFCQYFLLDIAFVLLLG 484
  
```

RESULT 3
 A39092

glucuronosyltransferase (EC 2.4.1.17) 1 precursor, bilirubin-specific - human
 N;Alternate names: bilirubin UDP-glucuronosyltransferase
 C;Species: Homo sapiens (man)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: A39092; E42586; A48887
 R;Ritter, J.K.; Crawford, J.M.; Owens, I.S.
 J. Biol. Chem. 266, 1043-1047, 1991
 A;Title: Cloning of two human liver bilirubin UDP-glucuronosyltransferase cDNAs with expression in COS-1 cells.
 A;Reference number: A39092; MUID:91093210; PMID:1898728
 A;Accession: A39092
 A;Molecule type: mRNA
 A;Residues: 1-533 <RIT>
 A;Cross-references: UNIPROT:P22309; GB:M57899; NID:g184472; PIDN:AAA63195.1; PID:g184473
 R;Ritter, J.K.; Chen, F.; Sheen, Y.Y.; Tran, H.M.; Kimura, S.; Yeatman, M.T.; Owens, I.S.
 J. Biol. Chem. 267, 3257-3261, 1992
 A;Title: A novel complex locus UGT1 encodes human bilirubin, phenol, and other UDP-glucuronosyltransferase isozymes with identical carboxyl termini.
 A;Reference number: A42586; MUID:92147680; PMID:1339448
 A;Accession: E42586
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-288 <RI2>
 A;Cross-references: GB:M84125; NID:g340131; PIDN:AAA61248.1; PID:g340132
 A;Note: sequence extracted from NCBI backbone (NCBIP:81433)
 R;Ritter, J.K.; Yeatman, M.T.; Kaiser, C.; Gridelli, B.; Owens, I.S.
 J. Biol. Chem. 268, 23573-23579, 1993
 A;Title: A phenylalanine codon deletion at the UGT1 gene complex locus of a Crigler-Najjar type I patient generates a pH-sensitive bilirubin UDP-glucuronosyltransferase.
 A;Reference number: A48887; MUID:94043159; PMID:8226884
 A;Accession: A48887
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 161-170,172-180 <RI3>
 A;Experimental source: liver, Crigler-Najjar type I patient
 A;Note: sequence extracted from NCBI backbone (NCBIP:138934)
 C;Genetics:
 A;Gene: GDB:UGT1A1; UGT1
 A;Cross-references: GDB:120007; OMIM:191740
 A;Map position: 2q37-2q37
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.5%; Score 679; DB 2; Length 533;
 Best Local Similarity 33.8%; Pred. No. 3.8e-45;
 Matches 175; Conservative 93; Mismatches 211; Indels 38; Gaps 13;

```

Qy      8 LLVGFL--PGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
          |::| || |::| |||| | |||::| | || ||::|
Db     11 LVLGLLLCVLGPVVS HAGKILLI-PVDGSHWLSMLGAIQQQLQQRGHEIVVL-----AP 62

Qy     66 D---FKKEEKSYQVISWLAPEDHQRE-FKKSF-----DFFLEETLGGRGKFENLL 111
          | : :: | : :: | ||| |::| | ||: : :: :
Db     63 DASLYIRDGAFTLTKTY--PVPFQREDVKESFVSLGHNVFENDSFLQRFVI---KTYKKIK 117

```


Qy 112 NVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFG 171
 | ||| |:|::| || :||::: : | | ::|: | | | |
 Db 118 KDSAMLLSGCSHLLHNKELMASLAESSFDVMLTDPFLPCSPIVAQYLSLPTVFFLHALPC 177

Qy 172 SLEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEH 228
 |||| | | |||| | :|| | |||| |: || : | : | :
 Db 178 SLEFEATQCPNPFYSYVPRPLSSHSDHMTFLQRVKNMLIAFSQNFLCDVVYSPY-ATLASE 236

Qy 229 FTEGSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIA 288
 | : : || | :| || | :|::|| |::||: | : | : | :
 Db 237 FLQ-REVTVQDLLSSASVWLFVRSDFVKDYPRPIMPNMVVFVGGINCLHQNPLSQEFAYIN 295

Qy 289 KFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKI 348
 | : | : : ||||: : : : | :| |::: : : : || | :
 Db 296 ASGEHGIVVFSLGSMVSEIPEKKAM-AIADALGKIPQTVLWRYTGT---RPSNLANNTIL 351

Qy 349 VDWLPQSDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfgdqpenmvrveakkfgv 408
 | ||||:|||| || | :|| | : : | :| :|||| :|||| :| | :| | ||
 Db 352 VKWLPQNDLLGHPMTRAFITHAGSHGVYESICNGVPMVMMPVLFQDQMDNAKRMETKGAGV 411

Qy 409 SIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGA 468
 :: : : : | | : | : : || || : | : : | : | | : : | : ||
 Db 412 TLNVLEMTSEDLENALKAVINDKSYKENIMRLSSLHKDRPVEPLDLAVFWVEFVMRHKGA 471

Qy 469 THLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWLWLCGK 505
 ||:| |::: || ||| : | :: |
 Db 472 PHLRPAHDLTWYQYHSLDVIGFLLAVVLTVAFITFK 508

RESULT 4

A40467

glucuronosyltransferase (EC 2.4.1.17) precursor - rat

N;Alternate names: UDP-glucuronosyltransferase isoform 53K

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 09-Jul-2004

C;Accession: A40467; A23520; S59627; A26064; I55247

R;Haque, S.J.; Petersen, D.D.; Nebert, D.W.; Mackenzie, P.I.

DNA Cell Biol. 10, 515-524, 1991

A;Title: Isolation, sequence, and developmental expression of rat UGT2B2: the gene encoding a constitutive UDP glucuronosyltransferase that metabolizes etiocholanolone and androsterone.

A;Reference number: A40467; MUID:91369480; PMID:1909872

A;Accession: A40467

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-530 <HAQ>

A;Cross-references: UNIPROT:P08541

R;Jackson, M.R.; Burchell, B.

Nucleic Acids Res. 14, 779-795, 1986

A;Title: The full length coding sequence of rat liver androsterone UDP-glucuronyltransferase cDNA and comparison with other members of this gene family.

A;Reference number: A23520; MUID:86120371; PMID:3003696

A;Accession: A23520

A;Molecule type: mRNA

A;Residues: 31-158,'E',160-285,'S',287-350,'I',352-362,'I',364-430,'E',432-530
<JAC>

Query Match 24.4%; Score 674.5; DB 2; Length 530;

Qy 34 SHYLLMDRVSQILQDHGHNVMTLNHKGPFMPDFKKEEKSYQVISW-LAPEDHQREFKKKS 92
||:::| | |::| : | ::| |::|

```

Db      381 LYEAIYHGIPMIGIPLFGDQPDNIAHMAVAKGAAVSLNIRTMSKLDFLSALVEVIDNPFYK 440
Qy      435 SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPWHEQYLFDFVVFLLG 494
          : | | | : | | | | : : : | | | : | | | |
Db      441 KNVMLLSTIHHDQPMKPLDRAVFWIEFIMRHKGAKHLRPLGHNLPWYQYHSLDVIGFLLT 500
Qy      495 LTLGTLWLTCGK-LLGMAVWWLRGARKVK 521
          | | | | : : : : : | : |
Db      501 CFAVIAALTVKCLLFMYRFFVKKEKKMK 528

```

RESULT 5

A42233

glucuronosyltransferase (EC 2.4.1.17) 2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 19-Jun-1992 #sequence_revision 18-Sep-1992 #text_change 09-Jul-2004

C;Accession: A42233; A24324

R;Mackenzie, P.I.; Rodbourn, L.

J. Biol. Chem. 265, 11328-11332, 1990

A;Title: Organization of the rat UDP-glucuronosyltransferase, UDPGTr-2, gene and characterization of its promoter.

A;Reference number: A42233; MUID:90293083; PMID:2113533

A;Accession: A42233

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-529 <MAC>

A;Cross-references: UNIPROT:P09875; GB:J05482

A;Note: the authors translated the codon GTA for residue 57 as B, and GTC for residue 116 as B

R;Mackenzie, P.I.

J. Biol. Chem. 261, 6119-6125, 1986

A;Title: Rat liver UDP-glucuronosyltransferase. Sequence and expression of a cDNA encoding a phenobarbital-inducible form.

A;Reference number: A24324; MUID:86196018; PMID:3084479

A;Accession: A24324

A;Molecule type: mRNA

A;Residues: 1-407,'V',409-529 <MA2>

A;Cross-references: GB:M13506; NID:g207580; PIDN:AAA42313.1; PID:g207581

A;Experimental source: liver

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 671; DB 2; Length 529;

Best Local Similarity 32.2%; Pred. No. 1.6e-44;

Matches 175; Conservative 90; Mismatches 228; Indels 50; Gaps 15;

```

Qy      6 VLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP 65
          : : | : : | | | : | | | : : : : | | | : :
Db      11 LIQLICYFRPGA----CGKVLVWPT-EYSHWINIKIILNELAQRGHEVTVLVSSASILIE 65
Qy      66 DFKKEEKSYQVISW-LAPEDHQREFKKSFDFFLE--ETLG---GRGKFENLLN----VLE 115
          | : : : : | | : | : | | : | | | : : | : |
Db      66 PTKESSINFEIYSVPLSKSDLEYSFAKWIDEWTRDFETLSIWYYYSKMVKVFNEYSQVVE 125
Qy      116 YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPVAILSTSFG---- 171
          | | : | : | | : | | : : : : | | | | |
Db      126 NL---CKALIWNKSLMKKLQGSQFDVILADAVGPCGELLAELLKTPLVYSLRFCPGYRCE 182

```

Qy 172 SLEFGLPIPLSYVPVFRSLLTDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHF 229
 |||:| |||| | |:| | | |||| | ::| | | : : : :
 Db 183 KFSGGLPLPPSYVPVVLSELSDRMTFVERVKNMLQMLYFDF-----WFQPFKEKSWSQFY 237

Qy 230 TE--GSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFI 287
 :: | | : : ||::| | : : :| | ||| :||| || ||::|::| | :
 Db 238 SDVLGRPTTLTEMMGKADIWLIRTFWDLEFPHFPLPNFDFVGGHLHCKPAKPLPREMEEFV 297

Qy 288 AKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCShWPKDVHLAANVK 347
 | : | | : : |||| | | : : | | : | | : | : | : | :
 Db 298 QSSGEHGVVVFSLGSMVKNL-TEEKANVVASALAQIPQKVVRFD---GKKPDTLGSNTR 353

Qy 348 IVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFG 407
 : |::|:| | | : | | | | | | | | | | | | | | | | | : : | |
 Db 354 LYKWIPQNDLLGHPKTKAFVAHGGTNGIYEAIYHGIPVGIPLFADQPDNINHMBAKGAA 413

Qy 408 VSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGG 467
 | : | | : | : | | | | : | | | | | : : | : : |
 Db 414 VRVDFSILSTTGLLTALKIVMNDPSYKENAMRLSRIHHDQPVKPLDRAVFWIEYVMRHKG 473

Qy 468 ATHLKPYVFQQPWHEQYLFDFVFLGLTLGT-----LWLCGKLLGMVWVWLRGARK 519
 | ||: : | : : || || : | | : | | | : |
 Db 474 AKHLRSTLHDLSWFQYHSLDVIGFLLLCVGVVFIITKFCLFCCRKTANM-----GKK 526

Qy 520 VKE 522
 ||
 Db 527 KKE 529

RESULT 6

B47113

glucuronosyltransferase (EC 2.4.1.17) UGT2B13 precursor - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: B47113

R;Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.

J. Biol. Chem. 268, 15260-15266, 1993

A;Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.

A;Reference number: A47113; MUID:93315511; PMID:8325897

A;Accession: B47113

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-531 <TUK>

A;Cross-references: UNIPROT:P36512; GB:L01081; NID:g165796; PIDN:AAA18020.1; PID:g165797

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 24.2%; Score 670; DB 2; Length 531;

Best Local Similarity 32.6%; Pred. No. 1.9e-44;

Matches 169; Conservative 90; Mismatches 206; Indels 54; Gaps 14;

Qy 34 SHYLLMDRVSQILQDHGHNVTML-----NHKRG----PFMPDFKKEEKSYQVISW 79
 ||::| : | || ||:| |::| | ::::| : |

```

Db      35 SHWMNMKTILDALVQQGHEVTVLRSSASIVIGSNNESGIKFETFHTSYRKDEIENFFMDW 94
Qy      80 LAPEDHQREFKKSFDFFLE---ETLGGRGKFENLLNVLEYLAL---QCSHFLNRKDIMDS 133
      :|  ::  :|  ||      :  ::|  :  |  :  | :|
Db      95 F-----YKMIYNVSIESYWETFS-----LTKMVILKYSDICEDICKEVILNKKLMTK 141
Qy     134 LKNENFDMVIVETFDYCPFLIAEKLGP-----FVAILSTSFGSLEFGLPIPLSYVPV 186
      |:  ||:::  :  |||  |  |  ||  :  |  ||  :|  ||||
Db     142 LQESRFDVVLADPVSPGGELLAELLKIPLVYSLRGFVGMYLQKHGG---GLLLPPSYVPV 198
Qy     187 FRSLTLDHMDFWGRVKNFL--MFFSFCRRQQHMQSTFDNTIKEHFTEGSRPV-LSHLLLK 243
      |  |  |  |  ||:|  |  ::|  |  :  :  :|  |  |||  |:  |
Db     199 MMSGGLGSQMTFMERVQNLLCVLYFDWF-FPKFNEKRWDQFYSEVL---GRPVTFLELMGK 254
Qy     244 AELWFINSDFAFDFARPLLNPNTVYVGGLMKPKPKVPQDLENFIAKFGDSGFVLVTLGSM 303
      |:|  |  |  :  :|  ||||  ::||  ||  ||:|:::|:  |:  |  |:  :|||
Db     255 ADMWLIRSYWDLEFPRPLLPNFDFIGGLHCKPAKPLPQEMEDFVQSSGEEGVVVFSLGSM 314
Qy     304 VNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSI 363
      ::  |  :  :|  |||  |:|  :  |  |  :|  ::  |:|:|  ||
Db     315 ISNL-TEERANVIASALAQLPQKVLWRFE---GKKPDMLGSNTRLYKWIPQNDLLGHPKT 370
Qy     364 RLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALK 423
      :  |:|  ||  |  :  |||  ||:|  |||  |:|  ::|  |  :  ||  :  :  |
Db     371 KAFITHGGANGVFEAIYHGIPMVGLPLFGDQLDNIVYMKAKGAAVKLNKLTMSADLLNA 430
Qy     424 MKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQOPWHEQ 483
      :|  ::  |  ||  |:  |  |  |:  |  |  ||:|:  ||  ||:  |:  :
Db     431 LKTVINDPYKENAMTSLRIHHDQPMKPLDRAVFWIEYVMRHKGAKHLRVAAHDLTWYQY 490
Qy     484 YLFDVFVFLGLTLGLTLWLCLGKLLGMAVWVWLRGARKVKE 522
      :  ||  ||  |  :|  |  :  ::  ||  |  :
Db     491 HSLDVIGFLLACVAITTYLIVKCCLLVYRYVLGAGKKKK 529

```

RESULT 7

C47113

glucuronosyltransferase (EC 2.4.1.17) UGT2B14 precursor - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: C47113

R;Tukey, R.H.; Pendurthi, U.R.; Nguyen, N.T.; Green, M.D.; Tephly, T.R.

J. Biol. Chem. 268, 15260-15266, 1993

A;Title: Cloning and characterization of rabbit liver UDP-glucuronosyltransferase cDNAs. Developmental and inducible expression of 4-hydroxybiphenyl UGT2B13.

A;Reference number: A47113; MUID:93315511; PMID:8325897

A;Accession: C47113

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-530 <TUK>

A;Cross-references: UNIPROT:P36513; GB:L01082; NID:g165798; PIDN:AAA18021.1;

PID:g165799

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match

23.9%; Score 662.5; DB 2; Length 530;

Matches 161; Conservative 75; Mismatches 209; Indels 21; Gaps 10;

RESULT 8

A35343

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Sep-1990 #sequence revision 14-Sep-1990 #text change 09-Jul-2004

C;Accession: A35343

R;Sato, H.; Koiwai, O.; Tanabe, K.; Kashiwamata, S.

Biochem. Biophys. Res. Commun. 169, 260-264, 1990

A;Title: Isolation and sequencing of rat liver bilirubin UDP-

glucuronosyltransferase cDNA: possible alternate splicing of a common primary transcript.

A;Reference number: A35343; MUID:90274676; PMID:2112380

A;Accession: A35343

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-531 <SAT>

A;Cross-references: UNIPROT:P20720; GB:M34007; NID:g207578; PIDN:AAA42312.1; PID:g207579

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 23.8%; Score 658; DB 2; Length 531;
Best Local Similarity 30.9%; Pred. No. 1.6e-43;
Matches 171; Conservative 106; Mismatches 211; Indels 66; Gaps 17;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60
      : |   |||:   ||   :|   |:| : : |||:| |   | : |   ||   :|
Db      7 LRGLSGLLLLLCALP---WAEGGKVL-VFPMEGSHWLSMRDVVRELHARGHQAVVL---- 58

Qy     61 GPFMPDFKKEEKSYQVISWLAP---EDHOREF----KKSFD-----FFLEETLGGRGK 106
      | :   | |   : : : : |   |:| ||   | | : |   ||   | |
Db     59 APEVTVMKGEDFFTLQTYAFPYTKEEYQREILGNAKKGFEPOHFVKTFE--ETMASIKK 116

Qy    107 FENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAIL 166
      | :|   |   | | : | : | : : | : : |||: : |   | :|: | | | |
Db    117 FFDL-----YANSCAALLHNKTLIQQLNSSSFVVLTDVPVPCGALLAKYLQIPAVFFL 170

Qy    167 STSFGSLEF---GLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFS---FCRRQQHMQST 220
      :   : : :   | | |||:|   :|:| || | | ||| | :   |   | : |
Db    171 RSVPCGIDYEATQCPKPSSYIPNLLTMLS DHMTFLQRVKNMLYPLTLKYIC----HLSIT 226

Qy    221 FDNTIKEHFTEGSR---PVLSHLLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIK 277
      : :   :   | |||   | :|   | | ||: ||: || | :|: || |
Db    227 PYESLASELLQREMSLVEVLSH---ASVWLFRGDFVFDYPRPIMPNMVFIGGINCVIKK 282

Qy    278 PVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP E I F K E M N N A F A H L P Q G V I W K C Q C S H W P 337
      | : | : | : :   | : | | : : ||| || :   :   | : |   : | | : | : :
Db    283 PLSQEF EAYVNASGEHGIVVFSLGS MVSEIPEKKAM-EIAEALGRIPQTL LWR YTG T --- 338

Qy    338 KDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPEN 397
      :   : || | : | | |||: || | | | : || | : | | : || || : || || | : |
Db    339 RPSNLAKNTILVKWLPQNDLLGH PKARAFITHSGSHGIYEGICNGVPMVMMP LFGDQMDN 398

Qy    398 MVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVG 457
      | : | : | | : : : : | : |   : | : : : | |   :   | : :   | : |
Db    399 AKRMETRGAGVT LNVLEMTADDLENALKTVINNKS YKENIMRLSSLHKDRPIEPLDLAVF 458

Qy    458 WIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFVLLGLTLGLTLWL-----CGKLLGM 509
      | : : | : : | | |||:|   | : : : | | ||| : |   : :   | | |
Db    459 WVEYVMRHKGAPHLRPA AHDLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG- 517

Qy    510 AVWWLRGARKVKET 523
      |   : || : :
Db    518 -----GKGRVKKS 525
```

RESULT 9

I57961

glucuronosyltransferase (EC 2.4.1.17) precursor - rat

N;Alternate names: glucuronosyltransferase 1 B1; morphine UGT

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004

C;Accession: I57961; S51197; S68333

R;Coffman, B.L.; Green, M.D.; King, C.D.; Tephly, T.R.

Mol. Pharmacol. 47, 1101-1105, 1995

A;Title: Cloning and stable expression of a cDNA encoding a rat liver UDP-glucuronosyltransferase (UDP-glucuronosyltransferase 1.1) that catalyzes the glucuronidation of opioids and bilirubin.

A;Reference number: I57961; MUID:95327065; PMID:7603447
 A;Accession: I57961
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-535 <RES>
 A;Cross-references: UNIPROT:Q64550; EMBL:U20551; NID:g695161; PIDN:AAC52219.1; PID:g695162
 R;Ishii, Y.; Tsuruda, K.; Tanaka, M.; Oguri, K.
 Arch. Biochem. Biophys. 315, 345-351, 1994
 A;Title: Purification of a phenobarbital-inducible morphine UDP-glucuronyltransferase isoform, absent from Gunn rat liver.
 A;Reference number: S51197; MUID:95077409; PMID:7986077
 A;Accession: S51197
 A;Molecule type: protein
 A;Residues: 30-41 <ISH>
 R;Ikushiro, S.; Emi, Y.; Iyanagi, T.
 Arch. Biochem. Biophys. 324, 267-272, 1995
 A;Title: Identification and analysis of drug-responsive expression of UDP-glucuronosyltransferase family 1 (UGT1) isozyme in rat hepatic microsomes using anti-peptide antibodies.
 A;Reference number: S68333; MUID:96132654; PMID:8554318
 A;Accession: S68333
 A;Molecule type: protein
 A;Residues: 30-37 <IKU>
 C;Genetics:
 A;Gene: UGT1.1
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.8%; Score 658; DB 2; Length 535;
 Best Local Similarity 31.4%; Pred. No. 1.7e-43;
 Matches 171; Conservative 97; Mismatches 215; Indels 62; Gaps 14;

Qy	13	LLPGVLL-----SEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP	65
		: : :	
Db	13	LLPCLLLCVLGPSASHAGKLLVI-PIDGSHWLSMLGVIQQLQQKGHEVVVI-----APEAS	67
Qy	66	DFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFEN---LLNVLE-----	115
		: : : : : : :	
Db	68	IHIKEGSFYTMRKYPVPFQENVTAA----FVEL---GRSVFDQDPFLLRVVKTYNKVKR	120
Qy	116	---YLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGS	172
		: : : : : : :	
Db	121	DSSMLLSGCShLLHNAEFMASLEQSHFDALLTDPFLPCGSIVAQYLSLPVAVYFLNALPCS	180
Qy	173	LEF---GLPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFS---FCRRQQHMQSTFDNTIK	226
		: : : : :	
Db	181	LDLEATQCPAPLSYVPKSLSSNTDRMNFQVRKNMIIALTENFLCRVVYSPYGSGLATEIL	240
Qy	227	EHFTEGSRPVLShLLKAEWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLENF	286
		: : : : : : : : : :	
Db	241	Q-----KEVTVKDLLSPASIWLNRNDFVKDYPRPIMPNMVFIGGINCLQKKALSQEFAY	295
Qy	287	IAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPPQGVWKCQCShWPKDVHLAANV	346
		: : : : : : : : :	
Db	296	VNASGEHGIVVFSLGSMVSEIPEKKAM-EIAEALGRIPQTVLWRYTGT---RPSNLAKNT	351

Qy 347 KIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKF 406
 :| ||||:|||| || | |:|| | : | | | :|||| | :|||| | :| :| :
 Db 352 ILVKWLPQNDLLGHPKARAFITHSGSHGIYEGICNGVPMVMPLFGDQMDNAKRMETRGA 411

Qy 407 GVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTG 466
 ||:: : :: |: | :| :: :| || : | : : |: | | |::|::
 Db 412 GVTNLVLEMTADDLENALKTVINNKSYPENIMRLSSLHKDRPIEPLDLAVFWVEYVMRHK 471

Qy 467 GATHLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWL-----CGKLLGMAVWWLRGAR 518
 || ||:| |: : || ||| : | :: | | |
 Db 472 GAPHLRPAADLTWYQYHSLDVIGFLLAIVLTVVFIVYKSCAYGCRKCFG-----GKG 524

Qy 519 KVKET 523
 :||::
 Db 525 RVKKS 529

RESULT 10

JN0619

glucuronosyltransferase (EC 2.4.1.17) 2B-4 precursor - human

N;Alternate names: UDP-glucuronosyltransferase 2B-11

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: JN0619; A27878

R;Jin, C.J.; Miners, J.O.; Lillywhite, K.J.; Mackenzie, P.I.

Biochem. Biophys. Res. Commun. 194, 496-503, 1993

A;Title: cDNA cloning and expression of two new members of the human liver UDP-glucuronosyltransferase 2B subfamily.

A;Reference number: JN0619; MUID:93326164; PMID:8333863

A;Accession: JN0619

A;Molecule type: mRNA

A;Residues: 1-528 <JIN>

A;Cross-references: UNIPROT:P06133; GB:AF081793; NID:g3426331

A;Experimental source: liver

R;Jackson, M.R.; McCarthy, L.R.; Harding, D.; Wilson, S.; Coughtrie, M.W.H.; Burchell, B.

Biochem. J. 242, 581-588, 1987

A;Title: Cloning of a human liver microsomal UDP-glucuronosyltransferase cDNA.

A;Reference number: A27878; MUID:87241362; PMID:3109396

A;Accession: A27878

A;Molecule type: mRNA

A;Residues: 1-108, 'F', 110-170, 'RP', 173-381, 'K', 383-384, 'SPR', 388-395, 'F', 397-528 <JAC>

A;Cross-references: GB:Y00317; NID:g37588; PIDN:CAA68415.1; PID:g37589

C;Genetics:

A;Gene: GDB:UGT2B4; UGT2B11

A;Cross-references: GDB:5891331; OMIM:600067

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-528/Product: glucuronosyltransferase 2B-11 #status predicted <MET>

F;492-509/Domain: transmembrane #status predicted <TMM>

F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

23.7%; Score 656.5; DB 2; Length 528;

Best Local Similarity 33.9%; Pred. No. 2.1e-43;

Matches 173; Conservative 85; Mismatches 213; Indels 39; Gaps 15;

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Qy      34 SHYLLMDRVSQILQDHGHNVTMLNHKRG----PFMPDFKKEEKSQVISWLAPEDHQREF 89
      ||:: : : | || ||:| | | | : | | ::
Db      34 SHWMNIKTILDELVQRGHEVTVLASSASISFDPNSPSTLKFEVYPVSLTKTEFEDIKQL 93

Qy      90 -----KKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDM 141
      | :| :| : | ::| | :| :| | : ||:
Db      94 VKRWAELPKDTFWSYLSQVQEIMWTFNDILRKF-----CKDIVSNKKLMKKLQESRFDV 147

Qy     142 VIVETFDYCPF--LIAEKLGKPFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLTDDHM 195
      |: : || |:|| | || | | | :| | | |||| | |:| |
Db     148 VLADA--VFPFGELLAELLKIPFVYSLRFSPGYAIEKHSGGLLFPPSYVPVVMSELSDQM 205

Qy     196 DFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAEWFINSDF 253
      | |||| ::::| | : | :| | | | | : ||:| | : :
Db     206 TFIERVKNMIYVLYFEFWFQIFDMKK-WDQFYSE--VLGRPTTLSETMAKADIWLIRNYW 262

Qy     254 AFDFARPLLNTVYVGGLMKPKIPVPQDLENFIAKFGDSGFVLVTLGSMV-NTCQNPEI 312
      | | |||| :||| || ||:|:::| | : |::| | : |||| | | : |
Db     263 DFQFPHPLLPNVEFVGGHLCKPAKPLPKEMEETFQSSGENGVVVFSLGSMVSNTSE--ER 320

Qy     313 FKEMNNAFAHLPQGVIWKCQCShWPkDVHlaANVKIvDWLPQSDLLAHPSIRLFVTHGGQ 372
      : :| | :|| |:|: : | | | : : |:|:| || | | :|||
Db     321 ANVIASALAKIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTRAFITHGGA 377

Qy     373 NSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKR 432
      | | ||| |:| |||:| | ||:|: :|| ||: : : | :| : : |
Db     378 NGIYEAIYHGIPMVGVPLLADQPDNIAHMKAKGAAVSLDFHTMSSTDLLNALKTVINDPL 437

Qy     433 YKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFVL 492
      || | : | | | : | | | | :|: || ||: | : : || ||
Db     438 YKENAMKLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRVAHDLTWFQYHSLDVTGFL 497

Qy     493 LGLTLGTLWLWLCGKLLGMAVW-WLRGARKVK 521
      | ::: | | || :| :| |
Db     498 LACVATVIFIITKCL-FCVWKVVRTGKKGK 526
```

RESULT 11

A35366

glucuronosyltransferase (EC 2.4.1.17) UDPGTh-2 precursor - human

C;Species: Homo sapiens (man)

C;Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 09-Jul-2004

C;Accession: A35366

R;Ritter, J.K.; Sheen, Y.Y.; Owens, I.S.

J. Biol. Chem. 265, 7900-7906, 1990

A;Title: Cloning and expression of human liver UDP-glucuronosyltransferase in COS-1 cells. 3,4-Catechol estrogens and estriol as primary substrates.

A;Reference number: A35366; MUID:90243659; PMID:2159463

A;Accession: A35366

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-529 <RIT>

A;Cross-references: UNIPROT:P16662; GB:J05428; NID:g340079; PIDN:AAA36793.1;

PID:g340080

C;Genetics:

A;Gene: GDB:UGT2B7; UGT2B9

A;Cross-references: GDB:5892203; OMIM:600218

A;Map position: 4q13-4q13

C;Superfamily: glucuronosyltransferase

C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

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Query Match          23.6%; Score 654.5; DB 2; Length 529;
Best Local Similarity 31.5%; Pred. No. 3.1e-43;
Matches 163; Conservative 88; Mismatches 212; Indels 55; Gaps 14;

Qy      34 SHYLLMDRVSQILQDGHNVNMLNHKRG-PFMPD-----FKKEEKSY---Q 75
      ||:: : : | || ||:| | : | | :: |
Db      34 SHWMNIKTILDELIQRGHEVTVLASSASILFDPNNSALKIEIYPTSLTKTELENFIMQQ 93

Qy      76 VISWL-APEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ-CSHFLNRKDIMDS 133
      : | | :| :| : : : :: : : | :: | |
Db      94 IKRWSDLPKD-----TFWLYFSQV-----QEIMSIFGDITRKFCCKDVVSNKKFMKK 139

Qy     134 LKNENFDMVIVETFDYCPFLIAEKLGPVFVAILSTS----FGSLEFGLPIPLSYVPVFRS 189
      :: ||:: : | | :|| || || | | | | | |
Db     140 VQESRFDVIFADAI FPCSELLAELFNI PFVYSLSFS PGYTFEKHSGGFIFPPSYVPVMS 199

Qy     190 LLTDHMDFWGRVKN--FLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLKA 244
      ||| | | ||| ::::| | || : | | | : ||
Db     200 ELTDQMTFMERVKNMIYVLYFDF-----WFEIFDMKKWDQFYSEVLGRPTTLSETMGKA 253

Qy     245 ELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMV 304
      ::| | : : | | |||| :||| || ||:::|:|: |::| | : ||||
Db     254 DVWLIRNSWNFQFPHPLLPNVDFVGGHLCKPAKPLPKEMEDFVQSSGENGVVVFSLGSMV 313

Qy     305 NTCQNPEIFKEMNNAFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIR 364
      : | : :| | :|| |:: : | | | : : |::|:| | | |
Db     314 SN-MTEERANVIASALAQIPQKVLWRFDGN---KPDTLGLNTRLYKWIPQNDLLGHPKTR 369

Qy     365 LFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
      |::||| | | ||| ||:||||||| |||:| :::| : : : | :
Db     370 AFITHGGANGIYEAIYHGIPMVGIPLFADQPDNIAHMKARGA AVRVDNTMSSTDLLNAL 429

Qy     425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQY 484
      |::: | || : | | : | | ||: |:: || ||: | : :
Db     430 KRVINDPSYKENVMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA AHDLTWFQYH 489

Qy     485 LFDVVFVLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522
      || ||| ::: , | : ||| | :
Db     490 SLDVIGFLLVCVATVIFIVTKCCLFCFW--KFARKAKK 525
```

RESULT 12

S15089

glucuronosyltransferase (EC 2.4.1.17) - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000

C;Accession: S15089

R;Lazard, D.; Zupko, K.; Poria, Y.; Nef, P.; Lazarovits, J.; Horn, S.; Khen, M.; Lancet, D.

Nature 349, 790-793, 1991

A;Title: Odorant signal termination by olfactory UDP glucuronosyl transferase.
A;Reference number: S15089; MUID:91156050; PMID:1900353
A;Accession: S15089
A;Molecule type: mRNA
A;Residues: 1-527 <LAZ>
A;Cross-references: GB:X57565; NID:g57762; PIDN:CAA40797.1; PID:g3980217
C;Superfamily: glucuronosyltransferase
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.5%; Score 650; DB 2; Length 527;
Best Local Similarity 31.2%; Pred. No. 6.9e-43;
Matches 166; Conservative 87; Mismatches 205; Indels 74; Gaps 12;

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Qy      7 LLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGPFMP- 65
      | | : | | | : |      | : | | : | : : |      | | | : |      | :
Db     12 LSLLGMSLGGNVL-----IWPMEGSHWLNVKIIDE LLRKEHNVTVLVASGALFITP 63

Qy     66 -----DFKKEE-----KSYQVISWL----APEDHQREFKKSFDFFLEETLGG 103
      | | | :      | : | : | |      : |      : | :      | |
Db     64 SVSPSLTFEIIYPVFPFGKEKIESVIKDF-VLTWLENRPSPTIWTIFYKEMAKVIEEFHLVS 122

Qy    104 RGKFENLLNVLEYLALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPV 163
      ||      |      | : : | | :      | : : : :      | : | | | | :
Db    123 RG-----ICDGV LKNEKLMTKLQRGKFVLLSDPVFPCGDIVALKLGIPFI 168

Qy    164 AILSTSFGSLEFG-----LPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCR 212
      | | |      : | | | | |      | | | | |      | | : | : :      |
Db    169 Y-----SLRFSPASTVEKHCGKVPFPSPSYVPAILSELTDQMSFADRVNRNFISY----R 217

Qy    213 RQQHMQSTFDNTIKEHFTE--GSRPVLSHLLLKAELWFINSDFAFDFARPLLNTVYVGG 270
      | : | |      : : : |      | : | | : | : : : | : | | | | : | |
Db    218 MQDYMFETLWKQWDSYYSKALGRPTTLCETMGKAEIWL MRTYWD FEFPRPYLPNFEFVGG 277

Qy    271 LMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIIWK 330
      | | | | : | : : | | :      | : | : | | | |      | : : | | : | :
Db    278 LHCKPAKPLPKEME EFVQTSGEHGVVVFSLGSMVKNL-TEEKANLIASALAQIPQKVLWR 336

Qy    331 CQC SHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPL 390
      :      | : | : : | | : | | | | | | | | | | | | | | : | :
Db    337 YK---GKIPATLGSNTRLFDWIPQNDLLGHPKTRAFITHGGTNGIYEAIYHGIPMVGVP 393

Qy    391 FGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLS 450
      | | | : | : : | | : : : | : : : : | | | : | |      | :
Db    394 FADQPDNIAHMKAKGA AVEVMNTMTSADLLSAVRVINEPFYKENAMRLSRIHHDQPVK 453

Qy    451 PTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLTLGLTLWL 502
      | | | | : | : : | | | :      | : : | | | |      : |
Db    454 PLDRAVFWIEFVMRHKGAKHLRVA AHDLSWFQYHSLDVIGFLLACMASAILL 505

```

RESULT 13

A48633

glucuronosyltransferase (EC 2.4.1.17) precursor - human

N;Alternate names: dihydrotestosterone/androstanediol UDP-glucuronosyltransferase isoform 3, udpgth-3; UDP glucuronosyltransferase 2 family, protein B15

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: A48633; I38559
 R;Chen, F.; Ritter, J.K.; Wang, M.G.; McBride, O.W.; Lubet, R.A.; Owens, I.S.
 Biochemistry 32, 10648-10657, 1993
 A;Title: Characterization of a cloned human dihydrotestosterone/androstenediol
 UDP-glucuronosyltransferase and its comparison to other steroid isoforms.
 A;Reference number: A48633; MUID:94002056; PMID:8399210
 A;Accession: A48633
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-530 <CHE>
 A;Cross-references: UNIPROT:P54855
 A;Experimental source: liver
 A;Note: sequence extracted from NCBI backbone (NCBIP:138786)
 R;Green, M.D.; Oturu, E.M.; Tephly, T.R.
 Drug Metab. Dispos. 22, 799-805, 1994
 A;Title: Stable expression of a human liver UDP-glucuronosyltransferase
 (UGT2B15) with activity toward steroid and xenobiotic substrates.
 A;Reference number: I38559; MUID:95136867; PMID:7835232
 A;Accession: I38559
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-530 <RES>
 A;Cross-references: EMBL:U08854; NID:g475758; PIDN:AAC50077.1; PID:g475759
 C;Genetics:
 A;Gene: GDB:UGT2B15; UGT2B8
 A;Cross-references: GDB:5892418; OMIM:600219
 A;Map position: 4q13-4q13
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 23.4%; Score 649; DB 2; Length 530;
 Best Local Similarity 31.8%; Pred. No. 8.3e-43;
 Matches 155; Conservative 90; Mismatches 218; Indels 24; Gaps 10;

Qy	34	SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEKSQVI-SWLAPEDHQREFKKS	92
		:: : : : : : :	
Db	34	SHWINMKTILEELVQRGHEVTVLTSASTLVNASKSSAIKLEVYPTSLTKNDLEDSLLKI	93
Qy	93	FDFLEETLGGRGKFENLLNVLEYLALQ-----CSHFLNRKDIMDSLKNENFDMVIV	144
		:: : : : : : : : : :	
Db	94	LDRWIYGV--SKNTFWSYFSQLQELCWEYYDYSNKLCKDAVLNKKLMMKLQESKFDVILA	151
Qy	145	ETFDYCPFLIAEKLKGPFVAILSTSFG-SLE---FGLPIPLSYVPVFRSLTLDHMDFWGR	200
		: : :: : :	
Db	152	DALNPCGELLAELFNIPFLYSLRFSVGYTFEKNGGGFLFPPSYVPVVMSELSQMI FMER	211
Qy	201	VKNF--LMFFSFCRRQHQMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWFINSDFAFDFA	258
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Qy	259	RPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN	318
		: : :: : :: : :: : : :	
Db	269	RPFLPNVDFVGGLHCKPAKPLPKEMEEFVQSSGENGIVVFSLGSMISN-MSEESANMIAS	327
Qy	319	AFAHLPQGVIVKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPsirLfvthggqnsimea	378
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Qy	31	VGGSHYLLMDRVSQILQD---HGHNVTMLNHKRGPFMPDFKKEEKSYQVISWLAPEDHQR	87
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Db	27	VWAAEYSLWMNMKTILKELVQRGHEVTVL-----ASSASIL--FDPNDSST	70
Qy	88	EFKKSDFDFLEETLGGRGKFENLLNLV-----EYLAALQ	120
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Db	71	LKLEVYPTSLTKT-----EFENIIMQLVKRLSEIQKDTFWLPFSQEQEILWAINDIIRNF	125
Qy	121	CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFG-SLE---FG	176
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Qy	177	LPIPLSYVPVFRSLLTDHMDFWGRVKN--FLMFFSFCRROOHMOSTFDNTIKEHFTEGSR	234

Db	186	FIFPPSYVPVMSKLSQMTFMERVKNMPLYVLYFDFWFQIFNMKK-WDQFYSE--VLGRP	242
Qy	235	PVLSHLLLKAEIWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSG	294
Db	243	TTLSETMRKADIWLMRNSWNFKFPHFPLPNVDFVGGGLHCKPAKPLPKEMEETFVQSSGENG	302
Qy	295	FVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCQSHWPKDVHLAANVKIVDWLPQ	354
Db	303	VVVFSLGSMVSN-MTEERANVIATALAKIPQKVLWRFDGN---KPDALGLNTRLYKWIPQ	358
Qy	355	SDLLAHPSIRLRFVTHGGQNSIMEAIQHGVPVMVGIPLFQDQPENMVRVEAKKFGVSIQLKK	414
Db	359	NDLLGHPKTRAFITHGGANGIYEAIYHGIPMVGIPLFFDQPDNIAHMKAKGA AVRVDENT	418
Qy	415	LKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKP	474
Db	419	MSSTDLLNALKTVINDPSYKENIMKLSRIQHDQPVKPLDRAVFWIEFVMRHKGAKHLRVA	478
Qy	475	VFQQPWHEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE	522
Db	479	AHNLTFWFQYHSLDVIGFLLACVATVLFIIITKCCFLCFW--KFARKGKK	524

RESULT 15

S07390

glucuronosyltransferase (EC 2.4.1.17) 3 precursor - rat

N;Alternate names: 17beta-hydroxysteroid UDP-glucuronosyltransferase; UDP-glucuronosyltransferase isoform 50K

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-May-1999

C;Accession: S07390; A33236; A28460; S59626

R;Harding, D.; Wilson, S.M.; Jackson, M.R.; Burchell, B.; Green, M.D.; Tephly, T.R.

Nucleic Acids Res. 15, 3936, 1987

A;Title: Nucleotide and deduced amino acid sequence of rat liver 17beta--hydroxysteroid UDP-glucuronosyltransferase.

A;Reference number: S07390; MUID:87231096; PMID:3108864

A;Accession: S07390

A;Molecule type: mRNA

A;Residues: 1-530 <HAR>

A;Cross-references: EMBL:Y00156

A;Experimental source: liver

A;Accession: A33236

A;Molecule type: protein

A;Residues: 24-61 <HAR2>

A;Experimental source: liver

R;Mackenzie, P.I.

J. Biol. Chem. 262, 9744-9749, 1987

A;Title: Rat liver UDP-glucuronosyltransferase. Identification of cDNAs encoding two enzymes which glucuronidate testosterone, dihydrotestosterone, and beta-estradiol.

A;Reference number: A28460; MUID:87250645; PMID:3110162

A;Accession: A28460

A;Molecule type: mRNA

A;Residues: 1-118,'G',120-240,'L',242-423,'S',425-499,'T',501-530 <MAC>

A;Experimental source: liver

R;Yamashita, A.; Watanabe, M.; Tonegawa, T.; Sugiura, T.; Waku, K.
 Biochem. J. 312, 301-308, 1995
 A;Title: Acyl-CoA binding and acylation of UDP-glucuronosyltransferase isoforms
 of rat liver: their effect on enzyme activity.
 A;Reference number: S59626; MUID:96077159; PMID:7492328
 A;Accession: S59626
 A;Molecule type: protein
 A;Residues: 24-44 <YAM>
 A;Experimental source: liver
 C;Superfamily: glucuronosyltransferase
 C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-530/Product: glucuronosyltransferase #status experimental <MAT>
 F;494-510/Domain: transmembrane #status predicted <TMM>

Query Match 23.1%; Score 640; DB 2; Length 530;
 Best Local Similarity 34.2%; Pred. No. 4.2e-42;
 Matches 167; Conservative 81; Mismatches 189; Indels 52; Gaps 15;

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Qy      34 SHYLLMDRVSQILQDHGHNV-----MLNHKRGPFMPDFKKEEKSYQVISWLAPEDH 85
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Db      34 SHWMNIKTILDELVQRGHEVTVLKPSAYYVLDPKKS---PDLKFETFPTSV----SKDEL 86

Qy      86 QREFKKSFDFFLEE-----TLGGRGKFENLLNVLE--YLALQCSHFLNRKDIMDSLKNEN 138
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Db      87 ENYFIKLVDVWTYELQRDTCLSYSPLLQNMIDEFSDYYLSL-CKDTVSNKQLMAKLQESK 145

Qy     139 FDMVIVETFDYCPFLIAEKLGPVAILSTSFSG-----SLEFGLPIPLSYVPVFRSLLT 192
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Db     146 FDVLLSDPVAACGELIAEVLHIPFLYSLRFSPGYKIEKSSGRFIL--PPSYVPVILSGMG 203

Qy     193 DHMDFWGRVKNFL--MFFSFCRRQQHM--QSTFDNTIKEHFTESRVPVLSHLLKAELEWF 248
      | | ||| : :| | || :| | | | : : ||:|
Db     204 GPMTFIDRVKNMICTLYFDF---WFHMFNAKKWDPFYSEIF--GRPTTLAETMGKAEMWL 258

Qy     249 INSDFAFDFARPLLNTVYVGGLMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQ 308
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Db     259 IRSYWDLEFPHPPTLPNVDIYIGGLQCRPPKPLPKDMEDFVQSSGEHGVVVFSLGSMVSS-- 316

Qy     309 NPEIFKEMNN----AFAHLPQGVIWKCQCSHWPKDVHLANVKIVDWLPQSDLLAHPSIR 364
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Db     317 ---MTEEKANAIAWALAQIPQKVLWKFD---GKTPATLGPNTRVYKWLQPNDLLGHPKTK 370

Qy     365 LFVTHGGQNSIMEAIQHGVPMVGIPLFQDQPENMVRVEAKKFGVSIQLKKLKAETLALKM 424
      ||||| | : ||| ||:|||||:|:| :|: : || |::: : | :
Db     371 AFVTHGGANGVYEAIIYHGIPMVGIPMFGEQHDNIAHMAKGAATVLTNIRTMSKTDLFNAL 430

Qy     425 KQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQY 484
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Db     431 KEIINNPFYKKNVWLSTIHHDQPMKPLDKAVFWIEFVMRHKGAKHLRPLGHDLPWYQYH 490

Qy     485 LFDVFVFL 493
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Db     491 SLDVIGFLL 499

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Search completed: February 15, 2005, 12:55:30

Job time : 61 secs

OM protein - protein search, using sw model

Run on: February 15, 2005, 07:50:18 ; Search time 95 Seconds
(without alignments)
1798.840 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
37	2768	100.0	523	14	US-10-013-909A-282	Sequence 282, App
66	2547	92.0	489	15	US-10-468-125-1	Sequence 1, Appli
67	2414	87.2	523	15	US-10-381-898-13	Sequence 13, Appl
68	2198	79.4	523	9	US-09-895-728-2	Sequence 2, Appli
69	2194	79.3	523	15	US-10-258-080-2	Sequence 2, Appli
70	2193	79.2	523	15	US-10-094-749-2927	Sequence 2927, Ap
71	2191	79.2	523	9	US-09-740-029-2	Sequence 2, Appli
72	1142	41.3	318	15	US-10-276-774-2663	Sequence 2663, Ap
73	963	34.8	221	15	US-10-104-047-2781	Sequence 2781, Ap
74	748.5	27.0	477	9	US-09-740-029-4	Sequence 4, Appli
75	716.5	25.9	527	9	US-09-962-678-2	Sequence 2, Appli
76	716.5	25.9	527	15	US-10-184-648-39	Sequence 39, Appl
77	714.5	25.8	527	9	US-09-981-353-166	Sequence 166, App
541	714.5	25.8	527	14	US-10-174-587-522	Sequence 522, App
591	714.5	25.8	527	15	US-10-258-080-1	Sequence 1, Appli
593	714.5	25.8	527	15	US-10-114-270-52	Sequence 52, Appl
600	713.5	25.8	527	15	US-10-114-270-50	Sequence 50, Appl
601	685.5	24.8	529	15	US-10-042-865-148	Sequence 148, App
602	685.5	24.8	529	15	US-10-072-012-506	Sequence 506, App
603	683.5	24.7	501	15	US-10-042-865-149	Sequence 149, App
604	683.5	24.7	501	15	US-10-072-012-835	Sequence 835, App
605	682	24.6	507	9	US-09-895-728-4	Sequence 4, Appli
606	682	24.6	507	9	US-09-962-678-4	Sequence 4, Appli
607	682	24.6	507	15	US-10-184-648-41	Sequence 41, Appl
608	679	24.5	533	9	US-09-981-353-152	Sequence 152, App
609	675.5	24.4	527	15	US-10-307-817-118	Sequence 118, App
610	670	24.2	529	15	US-10-468-125-6	Sequence 6, Appli
611	663.5	24.0	528	15	US-10-042-865-147	Sequence 147, App
612	663.5	24.0	528	15	US-10-072-012-505	Sequence 505, App
613	661.5	23.9	528	14	US-10-205-522-8	Sequence 8, Appli
614	661.5	23.9	528	15	US-10-042-865-145	Sequence 145, App
615	661.5	23.9	528	15	US-10-072-012-503	Sequence 503, App
616	656.5	23.7	528	15	US-10-042-865-146	Sequence 146, App
617	656.5	23.7	528	15	US-10-072-012-504	Sequence 504, App
618	655	23.7	530	15	US-10-381-898-6	Sequence 6, Appli
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624	653	23.6	527	14	US-10-235-994-28	Sequence 28, Appl
625	651.5	23.5	524	14	US-10-205-522-40	Sequence 40, Appl
626	649	23.4	530	14	US-10-205-522-113	Sequence 113, App
627	629	22.7	531	15	US-10-438-929-1	Sequence 1, Appli
628	623	22.5	530	16	US-10-408-765A-808	Sequence 808, App
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631	611	22.1	530	16	US-10-250-508-15	Sequence 15, Appl
632	608	22.0	530	16	US-10-250-508-17	Sequence 17, Appl
633	606	21.9	530	16	US-10-250-508-14	Sequence 14, Appl
634	603	21.8	530	16	US-10-250-508-16	Sequence 16, Appl
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636	521	18.8	454	13	US-10-060-311-2	Sequence 2, Appli
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638	503.5	18.2	288	13	US-10-060-311-3	Sequence 3, Appli
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644	380	13.7	245	9	US-09-305-856B-18	Sequence 18, Appl
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652	256	9.2	310	9	US-09-305-856B-14	Sequence 14, Appl
653	256	9.2	310	14	US-10-247-159-14	Sequence 14, Appl
654	255	9.2	289	9	US-09-305-856B-8	Sequence 8, Appli
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656	244.5	8.8	289	9	US-09-305-856B-4	Sequence 4, Appli
657	244.5	8.8	289	14	US-10-247-159-4	Sequence 4, Appli
658	239	8.6	129	9	US-09-738-973-36	Sequence 36, Appl
659	239	8.6	129	9	US-09-854-133-36	Sequence 36, Appl
660	239	8.6	129	14	US-10-144-649A-36	Sequence 36, Appl
661	227	8.2	317	9	US-09-305-856B-12	Sequence 12, Appl
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671	210.5	7.6	446	15	US-10-424-599-282136	Sequence 282136,
672	203.5	7.4	448	16	US-10-437-963-201110	Sequence 201110,
673	202.5	7.3	480	15	US-10-424-599-192321	Sequence 192321,
674	198.5	7.2	503	15	US-10-425-114-49497	Sequence 49497, A
675	198	7.2	444	15	US-10-424-599-271469	Sequence 271469,
676	198	7.2	482	16	US-10-437-963-136009	Sequence 136009,
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678	194	7.0	496	15	US-10-425-114-67279	Sequence 67279, A
679	190.5	6.9	511	9	US-09-773-882-11	Sequence 11, Appl
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681	189	6.8	72	9	US-09-864-761-41831	Sequence 41831, A
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683	188.5	6.8	506	16	US-10-203-295-4	Sequence 4, Appli
684	188.5	6.8	519	15	US-10-359-369-34	Sequence 34, Appl
685	187.5	6.8	504	15	US-10-359-369-31	Sequence 31, Appl
686	186	6.7	470	16	US-10-437-963-129470	Sequence 129470,
687	185.5	6.7	478	15	US-10-359-369-18	Sequence 18, Appl
688	185.5	6.7	484	15	US-10-359-369-8	Sequence 8, Appli
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690	183.5	6.6	321	15	US-10-425-114-49951	Sequence 49951, A
691	183	6.6	482	15	US-10-424-599-218783	Sequence 218783,
692	182.5	6.6	478	15	US-10-424-599-274039	Sequence 274039,
693	181.5	6.6	479	15	US-10-359-369-12	Sequence 12, Appl
694	181.5	6.6	479	15	US-10-203-319A-11	Sequence 11, Appl

695	178	6.4	483	15	US-10-424-599-258507	Sequence 258507,
696	177.5	6.4	313	15	US-10-424-599-193825	Sequence 193825,
697	177.5	6.4	511	15	US-10-359-369-22	Sequence 22, Appl
698	177.5	6.4	524	15	US-10-359-369-27	Sequence 27, Appl
699	177	6.4	447	15	US-10-424-599-215698	Sequence 215698,
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702	174.5	6.3	475	16	US-10-437-963-150992	Sequence 150992,
703	174.5	6.3	490	16	US-10-437-963-150172	Sequence 150172,
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705	173.5	6.3	508	16	US-10-437-963-138914	Sequence 138914,
706	173	6.2	430	15	US-10-229-148B-37	Sequence 37, Appl
707	171	6.2	218	15	US-10-424-599-280090	Sequence 280090,
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709	170.5	6.2	443	15	US-10-424-599-232416	Sequence 232416,
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713	169.5	6.1	527	15	US-10-424-599-269826	Sequence 269826,
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732	165	6.0	559	16	US-10-437-963-140683	Sequence 140683,
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734	164	5.9	458	16	US-10-437-963-104496	Sequence 104496,
735	164	5.9	496	16	US-10-437-963-180632	Sequence 180632,
736	163.5	5.9	228	15	US-10-424-599-186311	Sequence 186311,
737	163.5	5.9	388	15	US-10-425-114-42304	Sequence 42304, A
738	163.5	5.9	459	14	US-10-167-547C-24	Sequence 24, Appl
739	163.5	5.9	520	15	US-10-425-114-63886	Sequence 63886, A
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741	163	5.9	295	15	US-10-425-114-50700	Sequence 50700, A
742	163	5.9	308	16	US-10-767-701-38041	Sequence 38041, A
743	163	5.9	459	15	US-10-275-782-2	Sequence 2, Appli
744	163	5.9	484	15	US-10-424-599-185569	Sequence 185569,
745	163	5.9	486	15	US-10-425-114-50225	Sequence 50225, A
746	163	5.9	490	16	US-10-437-963-173247	Sequence 173247,
747	162.5	5.9	383	14	US-10-259-165-202	Sequence 202, App
748	162.5	5.9	473	15	US-10-424-599-282475	Sequence 282475,
749	162	5.9	416	16	US-10-437-963-142949	Sequence 142949,
750	162	5.9	482	16	US-10-437-963-133942	Sequence 133942,
751	162	5.9	485	16	US-10-437-963-117560	Sequence 117560,

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753	162	5.9	489	15	US-10-425-114-69280	Sequence 69280, A
754	162	5.9	497	15	US-10-425-114-53308	Sequence 53308, A
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757	161	5.8	144	15	US-10-424-599-284487	Sequence 284487,
758	161	5.8	167	15	US-10-424-599-197195	Sequence 197195,
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760	161	5.8	464	16	US-10-437-963-203793	Sequence 203793,
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762	161	5.8	479	15	US-10-424-599-272051	Sequence 272051,
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772	159.5	5.8	506	15	US-10-425-114-49468	Sequence 49468, A
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777	159	5.7	536	15	US-10-425-114-65018	Sequence 65018, A
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783	158	5.7	359	15	US-10-425-114-49044	Sequence 49044, A
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794	157	5.7	511	15	US-10-425-114-58985	Sequence 58985, A
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797	156	5.6	220	15	US-10-424-599-174823	Sequence 174823,
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804	155.5	5.6	440	16	US-10-437-963-108501	Sequence 108501,
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807	155	5.6	152	16	US-10-767-701-36217	Sequence 36217, A
808	155	5.6	470	16	US-10-437-963-190458	Sequence 190458,

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813	154	5.6	214	16	US-10-767-701-33387	Sequence 33387, A
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853	149	5.4	208	14	US-10-259-165-136	Sequence 136, App
854	149	5.4	306	15	US-10-424-599-151890	Sequence 151890,
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857	148.5	5.4	412	14	US-10-156-761-8483	Sequence 8483, Ap
858	148.5	5.4	471	16	US-10-437-963-176451	Sequence 176451,
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863	148	5.3	815	16	US-10-437-963-112487	Sequence 112487,
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874	146	5.3	207	15	US-10-425-114-52522	Sequence 52522, A
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877	146	5.3	504	16	US-10-437-963-173950	Sequence 173950,
878	146	5.3	772	16	US-10-437-963-152635	Sequence 152635,
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889	144	5.2	172	15	US-10-424-599-240150	Sequence 240150,
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891	144	5.2	454	16	US-10-437-963-133789	Sequence 133789,
892	144	5.2	498	16	US-10-437-963-134359	Sequence 134359,
893	144	5.2	656	15	US-10-424-599-179108	Sequence 179108,
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895	143.5	5.2	493	16	US-10-437-963-197508	Sequence 197508,
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907	142	5.1	506	15	US-10-424-599-201183	Sequence 201183,
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910	141.5	5.1	476	9	US-09-777-207-11	Sequence 11, Appl
911	141.5	5.1	476	13	US-10-078-929-201	Sequence 201, App
912	141.5	5.1	487	15	US-10-424-599-147435	Sequence 147435,
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917	141	5.1	480	16	US-10-437-963-194135	Sequence 194135,
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930	139	5.0	435	16	US-10-437-963-156531	Sequence 156531,
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942	137.5	5.0	431	10	US-09-941-947A-28	Sequence 28, Appl
943	137.5	5.0	431	14	US-10-218-118-4	Sequence 4, Appli
944	137.5	5.0	431	15	US-10-363-567-28	Sequence 28, Appl
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946	137.5	5.0	431	16	US-10-735-019-4	Sequence 4, Appli
947	137.5	5.0	431	16	US-10-848-307-2	Sequence 2, Appli
948	137.5	5.0	431	17	US-10-886-906-4	Sequence 4, Appli
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972	133	4.8	433	16	US-10-437-963-146479	Sequence 146479,
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974	132.5	4.8	455	15	US-10-424-599-196784	Sequence 196784,
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1244	91	3.3	1397	17	US-10-473-451-6	Sequence 6, Appli
1245	91	3.3	1826	15	US-10-289-762-113	Sequence 113, App
1246	90.5	3.3	99	16	US-10-767-701-55235	Sequence 55235, A
1247	90.5	3.3	364	15	US-10-369-493-11180	Sequence 11180, A
1248	90.5	3.3	381	15	US-10-369-493-1334	Sequence 1334, Ap
1249	90.5	3.3	602	10	US-09-953-067A-7	Sequence 7, Appli
1250	90.5	3.3	602	15	US-10-260-937-51	Sequence 51, Appl
1251	90.5	3.3	2111	16	US-10-437-963-112998	Sequence 112998,
1252	90.5	3.3	2783	15	US-10-369-493-6344	Sequence 6344, Ap
1253	90	3.3	106	16	US-10-767-701-55687	Sequence 55687, A
1254	90	3.3	304	15	US-10-424-599-183691	Sequence 183691,
1255	90	3.3	357	15	US-10-282-122A-61260	Sequence 61260, A
1256	90	3.3	357	15	US-10-282-122A-70571	Sequence 70571, A
1257	90	3.3	511	16	US-10-686-947-166	Sequence 166, App
1258	90	3.3	511	16	US-10-686-947-168	Sequence 168, App
1259	90	3.3	620	9	US-09-861-451A-34	Sequence 34, Appl
1260	90	3.3	838	14	US-10-084-839-2789	Sequence 2789, Ap
1261	90	3.3	1953	15	US-10-369-493-1945	Sequence 1945, Ap
1262	89.5	3.2	265	16	US-10-767-701-44289	Sequence 44289, A
1263	89.5	3.2	302	15	US-10-424-599-212485	Sequence 212485,
1264	89.5	3.2	422	15	US-10-335-977-7596	Sequence 7596, Ap

1265	89.5	3.2	422	15	US-10-335-977-7597	Sequence 7597, Ap
1266	89.5	3.2	426	15	US-10-335-977-7598	Sequence 7598, Ap
1267	89.5	3.2	596	15	US-10-112-944-404	Sequence 404, App
1268	89.5	3.2	665	15	US-10-108-260A-3396	Sequence 3396, Ap
1269	89.5	3.2	930	9	US-09-815-242-13481	Sequence 13481, A
1270	89.5	3.2	930	15	US-10-282-122A-74109	Sequence 74109, A
1271	89.5	3.2	1403	16	US-10-475-711-6	Sequence 6, Appli
1272	89.5	3.2	1420	16	US-10-475-711-8	Sequence 8, Appli
1273	89.5	3.2	1428	16	US-10-475-711-2	Sequence 2, Appli
1274	89.5	3.2	1445	16	US-10-475-711-4	Sequence 4, Appli
1275	89	3.2	678	15	US-10-282-122A-69719	Sequence 69719, A
1276	89	3.2	866	14	US-10-205-219-1	Sequence 1, Appli
1277	88.5	3.2	113	15	US-10-424-599-219817	Sequence 219817,
1278	88.5	3.2	198	15	US-10-424-599-250468	Sequence 250468,
1279	88.5	3.2	616	16	US-10-437-963-115230	Sequence 115230,
1280	88.5	3.2	620	16	US-10-408-765A-2886	Sequence 2886, Ap
1281	88.5	3.2	722	15	US-10-282-122A-71737	Sequence 71737, A
1282	88.5	3.2	726	10	US-09-932-257A-19	Sequence 19, Appl
1283	88.5	3.2	726	14	US-10-151-274-6	Sequence 6, Appli
1284	88.5	3.2	1561	15	US-10-369-493-1131	Sequence 1131, Ap
1285	88	3.2	374	15	US-10-369-493-13548	Sequence 13548, A
1286	88	3.2	388	14	US-10-138-701-57	Sequence 57, Appl
1287	88	3.2	430	15	US-10-084-846A-62	Sequence 62, Appl
1288	88	3.2	500	9	US-09-731-872-466	Sequence 466, App
1289	88	3.2	500	10	US-09-876-997-466	Sequence 466, App
1290	88	3.2	638	15	US-10-425-114-70558	Sequence 70558, A
1291	88	3.2	708	15	US-10-282-122A-68462	Sequence 68462, A
1292	88	3.2	838	10	US-09-864-636A-66	Sequence 66, Appl
1293	88	3.2	838	10	US-09-758-282-261	Sequence 261, App
1294	88	3.2	838	11	US-09-864-426A-66	Sequence 66, Appl
1295	88	3.2	838	14	US-10-084-839-66	Sequence 66, Appl
1296	88	3.2	979	15	US-10-360-522-58	Sequence 58, Appl
1297	88	3.2	1153	9	US-09-963-137-202	Sequence 202, App
1298	88	3.2	1153	10	US-09-962-854A-3	Sequence 3, Appli
1299	88	3.2	1153	10	US-09-963-131-202	Sequence 202, App
1300	88	3.2	1153	11	US-09-397-967-14	Sequence 14, Appl
1301	88	3.2	1948	16	US-10-437-963-137866	Sequence 137866,
1302	88	3.2	19723	15	US-10-084-846A-5	Sequence 5, Appli
1303	87.5	3.2	187	15	US-10-425-114-38952	Sequence 38952, A
1304	87.5	3.2	254	15	US-10-424-599-260301	Sequence 260301,
1305	87.5	3.2	305	15	US-10-282-122A-74291	Sequence 74291, A
1306	87.5	3.2	359	14	US-10-012-819-164	Sequence 164, App
1307	87.5	3.2	401	15	US-10-282-122A-52890	Sequence 52890, A
1308	87.5	3.2	432	9	US-09-881-752A-198	Sequence 198, App
1309	87.5	3.2	447	9	US-09-815-242-13490	Sequence 13490, A
1310	87.5	3.2	447	9	US-09-815-242-13612	Sequence 13612, A
1311	87.5	3.2	447	15	US-10-282-122A-74098	Sequence 74098, A
1312	87.5	3.2	472	15	US-10-282-122A-54597	Sequence 54597, A
1313	87.5	3.2	575	15	US-10-104-047-3622	Sequence 3622, Ap
1314	87.5	3.2	578	15	US-10-282-122A-44135	Sequence 44135, A
1315	87.5	3.2	623	15	US-10-296-115-1190	Sequence 1190, Ap
1316	87.5	3.2	824	16	US-10-437-963-194650	Sequence 194650,
1317	87.5	3.2	859	16	US-10-437-963-186692	Sequence 186692,
1318	87.5	3.2	896	16	US-10-437-963-180822	Sequence 180822,
1319	87.5	3.2	1452	16	US-10-408-765A-83	Sequence 83, Appl
1320	87	3.1	69	9	US-09-864-761-42081	Sequence 42081, A
1321	87	3.1	92	15	US-10-424-599-188790	Sequence 188790,

1322	87	3.1	356	14	US-10-161-398-6	Sequence 6, Appli
1323	87	3.1	356	14	US-10-161-398-7	Sequence 7, Appli
1324	87	3.1	356	15	US-10-424-599-152603	Sequence 152603,
1325	87	3.1	365	15	US-10-425-114-36617	Sequence 36617, A
1326	87	3.1	365	15	US-10-425-114-54709	Sequence 54709, A
1327	87	3.1	488	10	US-09-882-227-42	Sequence 42, Appl
1328	87	3.1	709	15	US-10-424-599-269773	Sequence 269773,
1329	87	3.1	735	16	US-10-437-963-162148	Sequence 162148,
1330	87	3.1	960	16	US-10-437-963-107065	Sequence 107065,
1331	87	3.1	1160	15	US-10-335-977-6136	Sequence 6136, Ap
1332	87	3.1	1167	9	US-09-815-242-11522	Sequence 11522, A
1333	87	3.1	1855	14	US-10-177-293-315	Sequence 315, App
1334	86.5	3.1	331	15	US-10-424-599-210688	Sequence 210688,
1335	86.5	3.1	352	9	US-09-815-242-13634	Sequence 13634, A
1336	86.5	3.1	359	15	US-10-282-122A-51853	Sequence 51853, A
1337	86.5	3.1	409	15	US-10-335-977-8277	Sequence 8277, Ap
1338	86.5	3.1	412	15	US-10-335-977-8278	Sequence 8278, Ap
1339	86.5	3.1	430	15	US-10-424-599-277805	Sequence 277805,
1340	86.5	3.1	443	15	US-10-424-599-147939	Sequence 147939,
1341	86.5	3.1	498	10	US-09-766-511B-26	Sequence 26, Appl
1342	86.5	3.1	498	14	US-10-189-123-51	Sequence 51, Appl
1343	86.5	3.1	498	14	US-10-188-495-51	Sequence 51, Appl
1344	86.5	3.1	498	15	US-10-424-233-7	Sequence 7, Appli
1345	86.5	3.1	542	15	US-10-289-762-496	Sequence 496, App
1346	86.5	3.1	591	10	US-09-766-511B-25	Sequence 25, Appl
1347	86.5	3.1	591	14	US-10-189-123-50	Sequence 50, Appl
1348	86.5	3.1	591	14	US-10-188-495-50	Sequence 50, Appl
1349	86.5	3.1	591	15	US-10-424-233-6	Sequence 6, Appli
1350	86.5	3.1	597	15	US-10-424-233-9	Sequence 9, Appli
1351	86.5	3.1	613	15	US-10-369-493-12123	Sequence 12123, A
1352	86.5	3.1	622	9	US-09-764-881-119	Sequence 119, App
1353	86.5	3.1	622	10	US-09-764-881-119	Sequence 119, App
1354	86.5	3.1	622	10	US-09-766-511B-23	Sequence 23, Appl
1363	86.5	3.1	622	14	US-10-116-252-13	Sequence 13, Appl
1423	86.5	3.1	622	14	US-10-189-123-48	Sequence 48, Appl

Search completed: February 15, 2005, 12:53:30
Job time : 102 secs

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OM protein - protein search, using sw model

Run on: February 15, 2005, 12:33:38 ; Search time 122 Seconds
(without alignments)
2195.225 Million cell updates/sec

Title: US-10-017-867A-282
Perfect score: 2768
Sequence: 1 MAGQRVLLLVGFLLPGVLLS.....GKLLGMAVWWLRGARKVKET 523

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2768	100.0	523	2	Q6UXC4	Q6uxc4 homo sapien
2	2754	99.5	523	2	Q8NBP2	Q8nbp2 homo sapien
3	2198	79.4	523	2	Q6NUS8	Q6nus8 homo sapien
4	2193	79.2	523	2	Q96DM6	Q96dm6 homo sapien
5	1815	65.6	523	2	Q8R0Y5	Q8r0y5 mus musculu
6	1804	65.2	523	2	Q8JZZ0	Q8jzz0 mus musculu
7	1802	65.1	523	2	Q8VC11	Q8vc11 m hypotheti
8	1145	41.4	523	2	Q63ZR6	Q63zr6 xenopus lae
9	963	34.8	221	2	Q8NAW4	Q8naw4 homo sapien
10	914.5	33.0	252	2	Q8IYS9	Q8iys9 homo sapien
11	792	28.6	302	2	Q8BRY7	Q8bry7 mus musculu
12	748.5	27.0	502	1	UDC1_RABIT	P36514 oryctolagus
13	727	26.3	541	2	Q98TB5	Q98tb5 gallus gall
14	714.5	25.8	527	2	Q6UWM9	Q6uwm9 homo sapien
15	699	25.3	541	1	CGT_HUMAN	Q16880 homo sapien

16	698	25.2	541	2	Q91W57	Q91w57	mus	musculu
17	697	25.2	541	1	CGT_MOUSE	Q64676	mus	musculu
18	689.5	24.9	529	2	Q9TSL6	Q9tsl6	macaca	fasc
19	685.5	24.8	529	2	O97951	O97951	macaca	fasc
20	685.5	24.8	534	2	Q8BWQ1	Q8bwq1	mus	musculu
21	684.5	24.7	498	2	Q9BDZ8	Q9bdz8	bos	taurus
22	684	24.7	541	1	CGT_RAT	Q09426	rattus	norv
23	681	24.6	530	2	Q9R110	Q9r110	cavia	porce
24	680.5	24.6	534	2	Q9D811	Q9d811	mus	musculu
25	680	24.6	529	2	Q9GLD9	Q9gld9	macaca	mula
26	679	24.5	533	1	UD11_HUMAN	P22309	homo	sapien
27	677.5	24.5	530	1	UDB2_RAT	P08541	rattus	norv
28	677.5	24.5	530	2	Q6K1J1	Q6k1j1	canis	famil
29	677.5	24.5	534	2	Q8R129	Q8r129	mus	musculu
30	676.5	24.4	533	2	Q6DHD1	Q6dhd1	brachydanio	
31	675.5	24.4	528	2	Q6PDD0	Q6pdd0	mus	musculu
32	674.5	24.4	530	2	Q7TT85	Q7tt85	rattus	norv
33	673.5	24.3	533	2	O46548	O46548	felis	silve
34	673	24.3	530	1	UDBK_MACFA	O77649	macaca	fasc
35	672.5	24.3	449	2	Q9H6S4	Q9h6s4	homo	sapien
36	670.5	24.2	528	2	Q80X89	Q80x89	mus	musculu
37	670	24.2	527	2	Q9ESE4	Q9ese4	mus	musculu
38	670	24.2	531	1	UDBD_RABIT	P36512	oryctolagus	
39	669	24.2	531	2	Q6T5F0	Q6t5f0	rattus	norv
40	669	24.2	535	1	UD11_MOUSE	Q63886	mus	musculu
41	669	24.2	535	2	Q6XL50	Q6xl50	mus	musculu
42	668	24.1	529	1	UDB1_RAT	P09875	rattus	norv
43	668	24.1	529	2	Q8R084	Q8r084	mus	musculu
44	667.5	24.1	529	2	Q8VIF8	Q8vif8	cavia	porce
45	667	24.1	533	2	O46549	O46549	felis	silve
46	666.5	24.1	528	2	Q8WN97	Q8wn97	macaca	fasc
47	665.5	24.0	533	2	O46423	O46423	felis	silve
48	665	24.0	531	1	UD15_RAT	Q64638	rattus	norv
49	665	24.0	533	2	Q9TSL7	Q9tsl7	macaca	fasc
50	664.5	24.0	528	1	UDBJ_MACFA	Q9xt55	macaca	fasc
51	664	24.0	531	2	Q8VD45	Q8vd45	rattus	norv
52	663.5	24.0	529	1	UDB9_MACFA	O02663	macaca	fasc
53	662.5	23.9	530	1	UDBE_RABIT	P36513	oryctolagus	
54	662	23.9	533	2	Q95KM4	Q95km4	macaca	mula
55	661.5	23.9	528	1	UDB4_HUMAN	P06133	homo	sapien
56	661	23.9	528	2	Q8VIF9	Q8vif9	cavia	porce
57	661	23.9	533	2	Q6T5F2	Q6t5f2	rattus	norv
58	660.5	23.9	529	2	Q9GLE0	Q9gle0	macaca	mula
59	658	23.8	533	1	UD12_RAT	P20720	rattus	norv
60	658	23.8	533	2	Q9BDG7	Q9bdg7	macaca	mula
61	658	23.8	535	1	UD11_RAT	Q64550	rattus	norv
62	657	23.7	530	1	UDBH_HUMAN	O75795	homo	sapien
63	654.5	23.6	529	1	UDB7_HUMAN	P16662	homo	sapien
64	654.5	23.6	529	2	Q6XL48	Q6xl48	mus	musculu
65	651.5	23.5	525	2	Q76K67	Q76k67	mus	musculu
66	651	23.5	527	1	UDA1_HUMAN	Q9y4x1	homo	sapien
67	651	23.5	529	2	Q6DJ94	Q6dj94	xenopus	tro
68	650.5	23.5	532	2	Q8K154	Q8k154	mus	musculu
69	650	23.5	527	1	UDA1_RAT	P36510	rattus	norv
70	649	23.4	523	1	UDBG_RABIT	O19103	oryctolagus	
71	649	23.4	530	1	UDBF_HUMAN	P54855	homo	sapien
72	648.5	23.4	530	2	Q6XL43	Q6xl43	mus	musculu

73	647	23.4	531	2	Q6T5F1	Q6t5f1	rattus norv
74	643	23.2	529	2	Q8BJL9	Q8bjl9	mus musculu
75	642	23.2	528	1	UDBA_HUMAN	P36537	homo sapien
76	642	23.2	531	1	UD13_RAT	Q64637	rattus norv
77	639	23.1	530	1	UDB6_RAT	P19488	rattus norv
78	639	23.1	533	1	UD12_MOUSE	P70691	mus musculu
79	638.5	23.1	532	1	UD16_HUMAN	P19224	homo sapien
80	637.5	23.0	530	1	UDB5_MOUSE	P17717	mus musculu
81	637.5	23.0	530	2	Q91WH2	Q91wh2	m riken cdn
82	637.5	23.0	532	2	Q8WUQ4	Q8wuq4	homo sapien
83	637	23.0	533	2	Q6XL49	Q6xl49	mus musculu
84	636.5	23.0	529	1	UDBS_HUMAN	Q9by64	homo sapien
85	635.5	23.0	529	2	O18736	O18736	bos taurus
86	635.5	23.0	530	2	Q8K169	Q8k169	mus musculu
87	635.5	23.0	530	2	Q68G19	Q68g19	rattus norv
88	635	22.9	534	1	UD15_HUMAN	P35504	homo sapien
89	634	22.9	530	1	UDB3_RAT	P08542	rattus norv
90	634	22.9	530	2	Q8VCN3	Q8vcn3	mus musculu
91	632.5	22.9	530	1	UDBC_RAT	P36511	rattus norv
92	632	22.8	528	2	Q6XL44	Q6xl44	mus musculu
93	631	22.8	530	1	UD18_HUMAN	Q9haw9	homo sapien
94	630.5	22.8	531	2	Q6XL45	Q6xl45	mus musculu
95	629	22.7	520	1	UD17_MOUSE	Q62452	mus musculu
96	627.5	22.7	531	2	Q6ZQM8	Q6zqm8	mus musculu
97	627	22.7	523	2	Q6DHS5	Q6dhs5	brachydanio
98	627	22.7	530	2	Q9TSM0	Q9tsm0	macaca fasc
99	625.5	22.6	535	2	Q6XA17	Q6xa17	branchiosto
100	624.5	22.6	532	2	Q9TSL9	Q9tsl9	macaca fasc
101	624.5	22.6	534	1	UD13_HUMAN	P35503	homo sapien
102	624	22.5	531	2	Q6T5E8	Q6t5e8	rattus norv
103	624	22.5	543	2	Q68G32	Q68g32	rattus norv
104	623.5	22.5	529	1	UDBB_HUMAN	O75310	homo sapien
105	623	22.5	531	1	UD17_RAT	Q64633	rattus norv
106	622	22.5	530	2	Q6T5E7	Q6t5e7	rattus norv
107	622	22.5	534	2	Q6XA18	Q6xa18	branchiosto
108	621	22.4	530	1	UD1A_HUMAN	Q9haw8	homo sapien
109	621	22.4	530	2	Q6NT91	Q6nt91	homo sapien
110	621	22.4	530	2	Q9TSL8	Q9tsl8	macaca fasc
111	620	22.4	531	2	Q8VD43	Q8vd43	rattus norv
112	619.5	22.4	528	2	Q95M37	Q95m37	canis famil
113	618	22.3	530	2	Q8VD44	Q8vd44	rattus norv
114	617.5	22.3	531	2	Q9XS55	Q9xs55	ovis aries
115	617	22.3	530	1	UD18_RAT	Q64634	rattus norv
116	615.5	22.2	531	2	Q6NSR5	Q6nsr5	mus musculu
117	615.5	22.2	532	1	UD14_RABIT	Q28612	oryctolagus
118	614.5	22.2	530	2	O18777	O18777	oryctolagus
119	614.5	22.2	531	2	Q8R0P3	Q8r0p3	mus musculu
120	614	22.2	530	1	UD12_HUMAN	P36509	homo sapien
121	614	22.2	530	2	Q6T5F3	Q6t5f3	rattus norv
122	612	22.1	530	1	UD17_HUMAN	Q9haw7	homo sapien
123	612	22.1	530	1	UD19_HUMAN	O60656	homo sapien
124	611.5	22.1	531	1	UD16_MOUSE	Q64435	mus musculu
125	611.5	22.1	532	2	Q9XS56	Q9xs56	ovis aries
126	608.5	22.0	530	2	Q6T5E9	Q6t5e9	rattus norv
127	608.5	22.0	531	2	Q6XL46	Q6xl46	mus musculu
128	607.5	21.9	530	2	P97886	P97886	rattus norv
129	607	21.9	531	2	Q6XL47	Q6xl47	mus musculu

130	606	21.9	534	1	UD14_HUMAN	P22310	homo sapien
131	600	21.7	526	2	Q7SXE7	Q7sxe7	brachydanio
132	600	21.7	529	1	UD16_RAT	P08430	rattus norv
133	596.5	21.5	531	1	UD16_RABIT	Q28611	oryctolagus
134	593	21.4	530	2	Q75XX1	Q75xx1	pleuronecte
135	590.5	21.3	530	1	UDB8_RAT	Q62789	rattus norv
136	584.5	21.1	530	2	Q9W710	Q9w710	pleuronecte
137	578.5	20.9	530	2	Q9W711	Q9w711	pleuronecte
138	561	20.3	511	2	Q7QC46	Q7qc46	anopheles g
139	551	19.9	526	2	Q7PTF6	Q7ptf6	anopheles g
140	549	19.8	529	2	Q7Q5T0	Q7q5t0	anopheles g
141	539	19.5	529	2	Q7Q5S9	Q7q5s9	anopheles g
142	538.5	19.5	472	1	UGT3_PLEPL	Q91280	pleuronecte
143	533	19.3	537	2	Q7QIR0	Q7qir0	anopheles g
144	528	19.1	310	2	Q6DFM6	Q6dfm6	xenopus tro
145	526	19.0	531	2	P70624	P70624	rattus norv
146	524	18.9	441	2	Q7Z6H8	Q7z6h8	homo sapien
147	521.5	18.8	504	2	Q7QGJ3	Q7qgj3	anopheles g
148	516	18.6	530	2	Q9VJ81	Q9vj81	drosophila
149	513	18.5	485	2	O96832	O96832	drosophila
150	513	18.5	516	2	Q9VGT0	Q9vgt0	drosophila
151	507	18.3	532	2	Q9W2J4	Q9w2j4	drosophila
152	506	18.3	516	2	Q9XYN3	Q9xyn3	drosophila
153	493.5	17.8	523	2	Q9VJI0	Q9vji0	drosophila
154	490.5	17.7	531	2	Q7Q3K0	Q7q3k0	anopheles g
155	488.5	17.6	493	2	Q9VDA5	Q9vda5	drosophila
156	488	17.6	527	2	Q965X5	Q965x5	caenorhabdi
157	480.5	17.4	518	2	Q7PT89	Q7pt89	anopheles g
158	476.5	17.2	531	2	Q7Q6N4	Q7q6n4	anopheles g
159	475	17.2	414	2	Q63662	Q63662	rattus norv
160	475	17.2	519	2	Q9VGT5	Q9vgt5	drosophila
161	475	17.2	534	2	Q9U3Q6	Q9u3q6	caenorhabdi
162	474.5	17.1	537	2	Q9VGS9	Q9vgs9	drosophila
163	474.5	17.1	537	2	Q9XYN4	Q9xyn4	drosophila
164	471	17.0	949	2	Q17399	Q17399	caenorhabdi
165	470.5	17.0	537	2	Q9VMG1	Q9vmg1	drosophila
166	469	16.9	524	2	Q8SYL7	Q8syl7	drosophila
167	464.5	16.8	543	2	Q8SZD9	Q8szd9	drosophila
168	462	16.7	491	2	Q9W2J3	Q9w2j3	drosophila
169	461	16.7	600	2	Q7Q4H4	Q7q4h4	anopheles g
170	458.5	16.6	543	2	Q9VJH8	Q9vjh8	drosophila
171	456	16.5	519	2	Q9VJ46	Q9vj46	drosophila
172	455.5	16.5	534	2	O01614	O01614	caenorhabdi
173	454.5	16.4	528	2	Q9VGT3	Q9vgt3	drosophila
174	454.5	16.4	530	2	O16276	O16276	caenorhabdi
175	454	16.4	517	2	Q9VJ45	Q9vj45	drosophila
176	453.5	16.4	521	2	Q9VGT4	Q9vgt4	drosophila
177	452.5	16.3	525	2	Q7QJN2	Q7qjn2	anopheles g
178	451	16.3	525	2	Q9VJ47	Q9vj47	drosophila
179	451	16.3	559	2	Q9VGT8	Q9vgt8	drosophila
180	450	16.3	500	2	Q7PIN9	Q7pin9	anopheles g
181	449	16.2	531	2	Q9TXZ4	Q9txz4	caenorhabdi
182	448	16.2	533	2	Q23323	Q23323	caenorhabdi
183	447.5	16.2	509	2	Q9VJH9	Q9vjh9	drosophila
184	447	16.1	531	2	Q21603	Q21603	caenorhabdi
185	445	16.1	487	2	Q9VGT2	Q9vgt2	drosophila
186	445	16.1	536	2	Q17813	Q17813	caenorhabdi

187	444	16.0	527	2	Q7QBV3	Q7qbv3	anopheles g
188	442	16.0	435	2	Q7KRQ7	Q7krq7	drosophila
189	442	16.0	485	2	Q7Q6N3	Q7q6n3	anopheles g
190	439	15.9	521	2	Q86S61	Q86s61	caenorhabdi
191	438	15.8	534	2	Q18629	Q18629	caenorhabdi
192	437	15.8	500	2	Q7PPY5	Q7ppy5	anopheles g
193	435	15.7	520	2	Q8WPG4	Q8wpg4	bombyx mori
194	434	15.7	521	2	Q9V9X9	Q9v9x9	drosophila
195	433	15.6	512	2	Q9VG29	Q9vg29	drosophila
196	430.5	15.6	527	2	Q9VGT1	Q9vgt1	drosophila
197	429	15.5	530	2	Q9VG30	Q9vg30	drosophila
198	429	15.5	760	2	Q7Q6N5	Q7q6n5	anopheles g
199	426	15.4	486	2	Q7PVZ4	Q7pvz4	anopheles g
200	425.5	15.4	530	2	Q7QIC1	Q7qic1	anopheles g
201	424	15.3	534	2	Q18636	Q18636	caenorhabdi
202	420.5	15.2	523	2	Q8MPX8	Q8mpx8	caenorhabdi
203	419	15.1	533	2	O01617	O01617	caenorhabdi
204	417	15.1	480	2	Q9VIM9	Q9vim9	drosophila
205	415.5	15.0	531	2	Q17404	Q17404	caenorhabdi
206	413	14.9	533	1	UGT5 CAEEL	Q20086	caenorhabdi
207	413	14.9	536	2	Q965U2	Q965u2	caenorhabdi
208	412.5	14.9	475	2	Q9TXZ3	Q9txz3	caenorhabdi
209	412.5	14.9	527	2	O01558	O01558	caenorhabdi
210	412.5	14.9	537	2	P91038	P91038	caenorhabdi
211	411	14.8	745	2	Q21706	Q21706	caenorhabdi
212	409.5	14.8	544	2	O44149	O44149	caenorhabdi
213	408	14.7	505	1	UGTF CAEEL	Q18081	caenorhabdi
214	408	14.7	533	2	O01616	O01616	caenorhabdi
215	407.5	14.7	522	2	Q18470	Q18470	caenorhabdi
216	405.5	14.6	520	2	Q18361	Q18361	caenorhabdi
217	400.5	14.5	498	2	Q7Q3K2	Q7q3k2	anopheles g
218	398.5	14.4	526	2	P91037	P91037	caenorhabdi
219	398	14.4	534	2	Q23336	Q23336	caenorhabdi
220	395.5	14.3	474	2	Q86S69	Q86s69	caenorhabdi
221	394.5	14.3	468	2	Q7Q3R0	Q7q3r0	anopheles g
222	392.5	14.2	500	2	Q95XQ5	Q95xq5	caenorhabdi
223	392.5	14.2	529	2	Q9TTY4	Q9tty4	caenorhabdi
224	391.5	14.1	530	2	Q93242	Q93242	caenorhabdi
225	390.5	14.1	540	2	Q9VCL3	Q9vcl3	drosophila
226	389	14.1	531	1	UGTE CAEEL	Q10941	caenorhabdi
227	386.5	14.0	542	2	O17757	O17757	caenorhabdi
228	385	13.9	532	2	Q9TTY5	Q9tty5	caenorhabdi
229	384	13.9	417	2	O01618	O01618	caenorhabdi
230	382	13.8	519	2	Q9VCL4	Q9vcl4	drosophila
231	382	13.8	532	2	Q9TXZ6	Q9txz6	caenorhabdi
232	380.5	13.7	535	2	O18009	O18009	caenorhabdi
233	379.5	13.7	535	2	Q23335	Q23335	caenorhabdi
234	379	13.7	322	2	Q8SZE2	Q8sze2	drosophila
235	377	13.6	524	2	O16506	O16506	caenorhabdi
236	375.5	13.6	525	1	UGTG CAEEL	Q22295	caenorhabdi
237	374	13.5	526	2	Q23333	Q23333	caenorhabdi
238	370.5	13.4	526	2	Q9VGS7	Q9vgs7	drosophila
239	368	13.3	539	2	Q9VCL5	Q9vcl5	drosophila
240	366.5	13.2	594	2	O16243	O16243	caenorhabdi
241	365	13.2	527	2	Q22770	Q22770	caenorhabdi
242	364.5	13.2	1003	2	Q18354	Q18354	caenorhabdi
243	362	13.1	529	2	Q17403	Q17403	caenorhabdi

244	361.5	13.1	533	2	Q23334	Q23334	caenorhabdi
245	361	13.0	531	2	P91039	P91039	caenorhabdi
246	360.5	13.0	531	2	Q9TXZ5	Q9txz5	caenorhabdi
247	358.5	13.0	369	2	Q6QQX7	Q6qqx7	homo sapien
248	354.5	12.8	540	2	O17756	O17756	caenorhabdi
249	350.5	12.7	515	2	O73553	O73553	spodoptera
250	349.5	12.6	515	2	Q8JPS2	Q8jps2	spodoptera
251	348.5	12.6	509	2	O91266	O91266	spodoptera
252	348.5	12.6	522	2	Q91BB3	Q91bb3	spodoptera
253	346.5	12.5	515	1	UDPE_NPVSL	Q88168	spodoptera
254	346.5	12.5	529	2	P91036	P91036	caenorhabdi
255	342.5	12.4	460	1	UDPE_GVLO	Q98166	lacanobia o
256	341	12.3	529	2	Q9VGS8	Q9vgs8	drosophila
257	339	12.2	558	2	Q19082	Q19082	caenorhabdi
258	338.5	12.2	490	2	Q9VM44	Q9vm44	drosophila
259	335.5	12.1	516	2	Q8JMB8	Q8jmb8	mamestra co
260	334	12.1	462	2	Q6QXI9	Q6qxi9	agrotis seg
261	333	12.0	506	2	Q21922	Q21922	caenorhabdi
262	332.5	12.0	523	2	Q9J8A8	Q9j8a8	spodoptera
263	331.5	12.0	528	1	UDPE_NPVM	Q83140	mamestra br
264	329	11.9	520	2	Q9WEV9	Q9wev9	ecotropis o
265	328.5	11.9	516	2	Q8QLJ5	Q8qlj5	mamestra co
266	328.5	11.9	516	2	Q71AH3	Q71ah3	mamestra co
267	328.5	11.9	525	2	Q6X859	Q6x859	spodoptera
268	328	11.8	560	2	Q9YMK2	Q9ymk2	lymantria d
269	326	11.8	515	2	O16988	O16988	caenorhabdi
270	325.5	11.8	512	2	Q80LH4	Q80lh4	adoxophyes
271	325.5	11.8	529	2	Q9W228	Q9w228	drosophila
272	325	11.7	463	2	Q7T5G5	Q7t5g5	cryptophleb
273	325	11.7	515	2	Q9E214	Q9e214	helicoverpa
274	324.5	11.7	446	2	Q91KX3	Q91kx3	epinotia ap
275	324	11.7	515	2	Q8JYS6	Q8jys6	helicoverpa
276	323	11.7	515	2	Q99GT6	Q99gt6	helicoverpa
277	322.5	11.7	513	2	O11454	O11454	buzura supp
278	322	11.6	515	2	O55264	O55264	heliiothis a
279	322	11.6	540	2	Q9GYR7	Q9gyr7	caenorhabdi
280	322	11.6	636	2	Q9VWV2	Q9vvw2	drosophila
281	321	11.6	515	2	O41856	O41856	helicoverpa
282	320	11.6	515	2	Q91BT6	Q91bt6	helicoverpa
283	318	11.5	527	2	O16922	O16922	caenorhabdi
284	317.5	11.5	541	2	O45109	O45109	caenorhabdi
285	317	11.5	593	2	O17401	O17401	caenorhabdi
286	316.5	11.4	488	1	UDPE_NPVLD	P41713	lymantria d
287	314.5	11.4	507	1	YKT6_CAEEL	P34317	caenorhabdi
288	313.5	11.3	582	2	Q7QCS2	Q7qcs2	anopheles g
289	311	11.2	524	1	UGTC_CAEEL	Q22181	caenorhabdi
290	304.5	11.0	294	2	Q9H3F9	Q9h3f9	homo sapien
291	303.5	11.0	537	2	Q9NBD8	Q9nbd8	drosophila
292	300.5	10.9	484	2	Q91ER4	Q91er4	cydia pomon
293	300.5	10.9	542	2	O16914	O16914	caenorhabdi
294	296	10.7	528	2	O16915	O16915	caenorhabdi
295	295.5	10.7	383	2	Q9N5N0	Q9n5n0	caenorhabdi
296	292	10.5	512	1	UGTB_CAEEL	Q22180	caenorhabdi
297	290.5	10.5	583	2	Q9I7T3	Q9i7t3	drosophila
298	290	10.5	429	2	Q9DVR5	Q9dvr5	plutella xy
299	283.5	10.2	527	2	O17123	O17123	caenorhabdi
300	281	10.2	448	2	Q999Y7	Q999y7	choristoneu

301	280	10.1	290	2	Q9R0A4	Q9r0a4	mus musculu
302	280	10.1	523	2	O16916	O16916	caenorhabdi
303	279	10.1	493	1	UDPE_NPVCD	Q90158	choristoneu
304	278	10.0	493	2	Q993S9	Q993s9	anticarsia
305	274.5	9.9	580	2	O16920	O16920	caenorhabdi
306	273.5	9.9	493	2	Q9VQT0	Q9vqt0	drosophila
307	270	9.8	405	2	Q94260	Q94260	caenorhabdi
308	270	9.8	434	2	Q8JRT0	Q8jrt0	phthorimaea
309	267	9.6	445	2	Q910F9	Q910f9	adoxophyes
310	267	9.6	445	2	Q77IS9	Q77is9	adoxophyes
311	264.5	9.6	501	2	O16322	O16322	caenorhabdi
312	260.5	9.4	397	2	Q7QDP0	Q7qdp0	anopheles g
313	260	9.4	389	2	Q8DSH9	Q8dsh9	streptococc
314	259.5	9.4	489	1	UDPE_NPVOP	Q65363	orgyia pseu
315	256	9.2	310	2	Q13460	Q13460	homo sapien
316	256	9.2	492	2	O89808	O89808	epiphyas po
317	256	9.2	506	2	Q9GZD1	Q9gzd1	caenorhabdi
318	250	9.0	506	2	Q913H6	Q913h6	bombyx mori
319	248	9.0	506	2	O92382	O92382	bombyx mori
320	247.5	8.9	275	2	Q63841	Q63841	mus sp. udp
321	246.5	8.9	506	1	UDPE_NPVAC	P18569	autographa
322	244	8.8	581	2	P91326	P91326	caenorhabdi
323	242.5	8.8	795	2	Q19222	Q19222	caenorhabdi
324	242	8.7	491	1	UDPE_NPVCF	Q90157	choristoneu
325	241	8.7	285	2	Q13406	Q13406	homo sapien
326	240.5	8.7	287	2	Q8WX91	Q8wx91	homo sapien
327	240	8.7	287	2	Q8WX90	Q8wx90	homo sapien
328	240	8.7	287	2	Q75XT5	Q75xt5	homo sapien
329	238.5	8.6	287	2	Q75XT3	Q75xt3	homo sapien
330	238	8.6	400	2	Q739H3	Q739h3	bacillus ce
331	237	8.6	284	2	Q9H3G0	Q9h3g0	homo sapien
332	237	8.6	285	2	Q96PP1	Q96pp1	homo sapien
333	236	8.5	287	2	Q8WX89	Q8wx89	homo sapien
334	234	8.5	284	2	Q9H3G1	Q9h3g1	homo sapien
335	234	8.5	285	2	Q96PN9	Q96pn9	homo sapien
336	232.5	8.4	506	2	Q8B9N4	Q8b9n4	rachiplusia
337	232	8.4	402	2	Q6HJP7	Q6hjp7	bacillus th
338	229	8.3	284	2	Q9H3G2	Q9h3g2	homo sapien
339	229	8.3	285	2	Q96PP0	Q96pp0	homo sapien
340	228.5	8.3	402	2	Q81RG4	Q81rg4	bacillus an
341	227.5	8.2	400	2	Q735L3	Q735l3	bacillus ce
342	227	8.2	317	2	Q13407	Q13407	homo sapien
343	226	8.2	285	2	Q64671	Q64671	rattus norv
344	226	8.2	402	2	Q63C86	Q63c86	bacillus ce
345	225.5	8.1	402	2	Q81EB6	Q81eb6	bacillus ce
346	225	8.1	370	2	Q8MNX7	Q8mnx7	caenorhabdi
347	223	8.1	153	1	UD21_RAT	P19489	rattus norv
348	222.5	8.0	283	2	Q9BG60	Q9bg60	mustela put
349	222.5	8.0	370	2	Q8IA78	Q8ia78	caenorhabdi
350	222	8.0	287	2	Q8WX86	Q8wx86	homo sapien
351	222	8.0	287	2	Q8WX87	Q8wx87	homo sapien
352	222	8.0	287	2	Q8WX88	Q8wx88	homo sapien
353	221.5	8.0	397	2	Q736S5	Q736s5	bacillus ce
354	220	7.9	485	2	Q9Q3Y1	Q9q3y1	amsacta alb
355	210.5	7.6	309	2	Q8T744	Q8t744	branchiosto
356	206	7.4	460	2	Q6T2C3	Q6t2c3	streptomyce
357	203.5	7.4	448	2	Q9AUV4	Q9auv4	oryza sativ

358	202	7.3	397	2	Q81CG5	Q81cg5	bacillus ce
359	199	7.2	458	2	Q6W5Q9	Q6w5q9	streptomyce
360	198	7.2	482	2	Q6YZQ6	Q6yzq6	oryza sativ
361	197.5	7.1	488	2	Q9LXV0	Q9lxv0	arabidopsis
362	192	6.9	458	2	Q9EWA4	Q9ewa4	streptomyce
363	191.5	6.9	448	2	Q9SBQ3	Q9sbq3	petunia hyb
364	190.5	6.9	431	2	Q7N615	Q7n615	photorhabdu
365	190	6.9	511	1	LGT_CITUN	Q9mb73	citrus unsh
366	189.5	6.8	446	2	Q83WG5	Q83wg5	streptomyce
367	188.5	6.8	506	2	Q9L4W6	Q9l4w6	streptomyce
368	187	6.8	447	2	O04114	O04114	perilla fru
369	187	6.8	461	2	Q8S3B9	Q8s3b9	glycine max
370	187	6.8	462	2	Q9FUJ6	Q9fuj6	phaseolus v
371	187	6.8	480	2	Q7XHR3	Q7xhr3	oryza sativ
372	186.5	6.7	488	2	Q8VZF9	Q8vzf9	arabidopsis
373	186.5	6.7	490	2	Q8H0V7	Q8h0v7	arabidopsis
374	186	6.7	419	2	P72650	P72650	synechocyst
375	185.5	6.7	455	2	Q9ZWS2	Q9zws2	vigna mungo
376	185.5	6.7	484	2	O23400	O23400	arabidopsis
377	185	6.7	143	2	Q98TP0	Q98tp0	platichthys
378	185	6.7	433	1	UFOG_SOLME	Q43641	solanum mel
379	184.5	6.7	453	2	Q9SYK9	Q9syk9	arabidopsis
380	184	6.6	462	2	Q8S998	Q8s998	phaseolus a
381	182.5	6.6	456	2	Q9AR43	Q9ar43	vitis vinif
382	182.5	6.6	456	2	Q9AR45	Q9ar45	vitis vinif
383	182	6.6	271	2	Q9N962	Q9n962	leishmania
384	182	6.6	413	1	CRTX_ERWHE	Q01330	erwinia her
385	182	6.6	449	2	Q8LKT1	Q8lkt1	sorghum bic
386	182	6.6	453	1	UFOG_GENTR	Q96493	gentiana tr
387	181.5	6.6	449	2	O22822	O22822	arabidopsis
388	181.5	6.6	456	2	Q9AQV0	Q9aqv0	vitis vinif
389	181.5	6.6	460	2	Q6VAA6	Q6vaa6	stevia reba
390	181.5	6.6	479	2	O23401	O23401	arabidopsis
391	181	6.5	449	2	Q8LKT3	Q8lkt3	sorghum bic
392	181	6.5	555	2	Q66PF4	Q66pf4	fragaria an
393	180.5	6.5	259	2	O16507	O16507	caenorhabdi
394	180.5	6.5	288	2	Q8LM15	Q8lm15	oryza sativ
395	180	6.5	479	2	Q8LB44	Q8lb44	arabidopsis
396	180	6.5	482	2	Q69JH3	Q69jh3	oryza sativ
397	180	6.5	483	2	Q93NW9	Q93nw9	streptomyce
398	179	6.5	565	2	Q9LSY5	Q9lsy5	arabidopsis
399	178.5	6.4	456	2	O22304	O22304	vitis vinif
400	178	6.4	428	2	P95134	P95134	mycobacteri
401	177	6.4	405	2	O31853	O31853	bacillus su
402	177	6.4	457	2	Q9SKC1	Q9skc1	arabidopsis
403	177	6.4	460	2	Q6X1C0.....	Q6x1c0	crocus sati
404	177	6.4	481	2	Q8GS49	Q8gs49	oryza sativ
405	176.5	6.4	1184	2	Q9SYK8	Q9syk8	arabidopsis
406	176	6.4	463	2	Q50458	Q50458	mycobacteri
407	175.5	6.3	396	2	Q65JC2	Q65jc2	bacillus li
408	175.5	6.3	452	2	O22303	O22303	vitis vinif
409	175.5	6.3	480	1	HQGT_ARATH	Q9ml56	arabidopsis
410	175	6.3	478	2	Q94IF2	Q94if2	nicotiana t
411	175	6.3	555	2	Q84UE9	Q84ue9	fragaria an
412	174.5	6.3	431	2	Q8VUJ7	Q8vuj7	pantoea agg
413	174.5	6.3	456	2	Q9AVK6	Q9avk6	vitis labru
414	174.5	6.3	456	2	Q9AVK7	Q9avk7	vitis labru

415	174.5	6.3	482	2	Q6Z688	Q6z688	oryza sativ
416	174.5	6.3	490	2	Q6AUC5	Q6auc5	oryza sativ
417	174.5	6.3	496	2	Q6Z481	Q6z481	oryza sativ
418	174	6.3	402	2	Q8KUH5	Q8kuh5	actinosynne
419	173.5	6.3	431	1	CRTX_PANAN	P21686	pantoea ana
420	173.5	6.3	458	2	Q7XI34	Q7xi34	oryza sativ
421	172.5	6.2	390	2	Q8S9A8	Q8s9a8	phaseolus a
422	172.5	6.2	462	2	Q8S3B5	Q8s3b5	phaseolus l
423	172	6.2	394	2	Q62YM9	Q62ym9	bacillus li
424	172	6.2	468	2	Q9SBQ2	Q9sbq2	petunia hyb
425	172	6.2	476	2	Q9LML7	Q9lml7	arabidopsis
426	171.5	6.2	464	2	Q8S3B8	Q8s3b8	glycine max
427	171	6.2	452	2	O48715	O48715	arabidopsis
428	171	6.2	467	2	O82383	O82383	arabidopsis
429	171	6.2	473	2	Q8LKG3	Q8lkg3	stevia reba
430	171	6.2	474	2	Q6R129	Q6r129	citrus sine
431	171	6.2	478	2	Q942C4	Q942c4	oryza sativ
432	170.5	6.2	450	2	Q89RS0	Q89rs0	bradyrhizob
433	170.5	6.2	471	2	Q942C3	Q942c3	oryza sativ
434	170.5	6.2	479	2	Q94IF1	Q94if1	nicotiana t
435	169.5	6.1	449	2	Q9LS16	Q9ls16	arabidopsis
436	169.5	6.1	454	2	Q9XF16	Q9xf16	forsythia i
437	169.5	6.1	456	2	Q8LFR6	Q8lfr6	arabidopsis
438	169.5	6.1	459	2	Q9LFK0	Q9lfk0	arabidopsis
439	169.5	6.1	483	2	Q6VAA4	Q6vaa4	stevia reba
440	169.5	6.1	487	2	Q9LME8	Q9lme8	arabidopsis
441	169	6.1	395	2	Q65N79	Q65n79	bacillus li
442	169	6.1	456	2	O22182	O22182	arabidopsis
443	169	6.1	457	2	Q9AUV3	Q9auv3	oryza sativ
444	168.5	6.1	456	2	Q9SKC5	Q9skc5	arabidopsis
445	168.5	6.1	492	2	Q8LM13	Q8lml3	oryza sativ
446	168	6.1	470	2	Q8S9A4	Q8s9a4	phaseolus a
447	168	6.1	478	2	Q66PF3	Q66pf3	fragaria an
448	167.5	6.1	391	2	Q8L5N2	Q8l5n2	malus domes
449	167.5	6.1	397	2	Q8KNE0	Q8kne0	micromonosp
450	167.5	6.1	475	2	O23402	O23402	arabidopsis
451	167.5	6.1	479	2	Q9LSY6	Q9lsy6	arabidopsis
452	167	6.0	93	2	Q9NS17	Q9ns17	homo sapien
453	167	6.0	474	2	Q8S9A6	Q8s9a6	phaseolus a
454	166.5	6.0	462	2	Q7XWK3	Q7xwk3	oryza sativ
455	166.5	6.0	466	2	Q66PF5	Q66pf5	fragaria an
456	166.5	6.0	483	2	Q9XES4	Q9xes4	malus domes
457	166.5	6.0	484	2	Q6ER37	Q6er37	oryza sativ
458	166	6.0	280	2	Q9ZWQ4	Q9zwq4	vigna mungo
459	166	6.0	460	2	O48676	O48676	arabidopsis
460	166	6.0	465	2	Q8LKT4	Q8lkt4	sorghum bic
461	166	6.0	518	2	Q7XWV5	Q7xwv5	oryza sativ
462	165.5	6.0	407	2	Q9S1V2	Q9slv2	streptomyce
463	165.5	6.0	451	2	Q9SBQ8	Q9sbq8	petunia hyb
464	165.5	6.0	462	2	O04622	O04622	arabidopsis
465	165.5	6.0	477	2	Q9ZWQ5	Q9zwq5	vigna mungo
466	165	6.0	445	2	Q7XHS6	Q7xhs6	oryza sativ
467	165	6.0	485	2	Q6VAA8	Q6vaa8	stevia reba
468	165	6.0	493	2	Q6EP59	Q6ep59	oryza sativ
469	164.5	5.9	435	2	Q98EL2	Q98el2	rhizobium l
470	164.5	5.9	449	2	O22820	O22820	arabidopsis
471	164.5	5.9	461	2	Q9ZR25	Q9zr25	verbena x h

472	164.5	5.9	462	2	Q8S3B6	Q8s3b6	phaseolus l
473	164.5	5.9	472	2	Q9LFJ9	Q9lfj9	arabidopsis
474	164.5	5.9	492	2	Q7XKH9	Q7xkh9	oryza sativ
475	164.5	5.9	500	2	Q69JH2	Q69jh2	oryza sativ
476	164	5.9	458	2	Q8RU64	Q8ru64	oryza sativ
477	164	5.9	471	1	IAAG_MAIZE	Q41819	zea mays (m
478	164	5.9	478	2	Q9S7R8	Q9s7r8	arabidopsis
479	164	5.9	487	2	Q94A84	Q94a84	arabidopsis
480	164	5.9	487	2	Q7XJ52	Q7xj52	allium cepa
481	164	5.9	496	2	Q7XTG9	Q7xtg9	oryza sativ
482	163.5	5.9	457	2	O23205	O23205	arabidopsis
483	163.5	5.9	470	2	Q8RU71	Q8ru71	nicotiana t
484	163.5	5.9	471	1	UFO1_MAIZE	P16166	zea mays (m
485	163.5	5.9	471	2	Q84XC2	Q84xc2	zea mays (m
486	163	5.9	361	2	Q6X3X7	Q6x3x7	ipomoea pur
487	163	5.9	361	2	Q6X3X8	Q6x3x8	ipomoea nil
488	163	5.9	452	2	Q76G23	Q76g23	aralia cord
489	163	5.9	459	1	ZOG_PHALU	Q9zsk5	phaseolus l
490	163	5.9	486	2	Q84ZE0	Q84ze0	oryza sativ
491	163	5.9	490	2	Q7XHS0	Q7xhs0	oryza sativ
492	162.5	5.9	404	2	Q62XT4	Q62xt4	bacillus li
493	162.5	5.9	406	2	Q65ME1	Q65me1	bacillus li
494	162.5	5.9	420	2	O22603	O22603	ipomoea pur
495	162.5	5.9	453	2	Q9SNB2	Q9snb2	arabidopsis
496	162.5	5.9	457	2	Q8LKT6	Q8lkt6	sorghum bic
497	162.5	5.9	458	2	Q94AB5	Q94ab5	arabidopsis
498	162.5	5.9	466	2	Q947K4	Q947k4	brassica na
499	162.5	5.9	484	2	Q8LJ11	Q8lj11	oryza sativ
500	162	5.9	464	2	Q9M051	Q9m051	arabidopsis
501	162	5.9	485	2	Q6Z684	Q6z684	oryza sativ
502	161.5	5.8	450	2	Q9FIA0	Q9fia0	arabidopsis
503	161.5	5.8	471	2	Q8S995	Q8s995	phaseolus a
504	161.5	5.8	487	2	Q7XSX9	Q7xsx9	oryza sativ
505	161	5.8	454	1	ZOX_PHAVU	P56725	phaseolus v
506	161	5.8	459	2	Q9M6E7	Q9m6e7	nicotiana t
507	161	5.8	463	2	Q8H3T8	Q8h3t8	oryza sativ
508	161	5.8	474	2	O82382	O82382	arabidopsis
509	161	5.8	476	2	Q7XTH0	Q7xth0	oryza sativ
510	161	5.8	1198	2	Q06321	Q06321	saccharomyc
511	160.5	5.8	472	2	Q8LR91	Q8lr91	oryza sativ
512	160.5	5.8	495	2	Q8S9A0	Q8s9a0	phaseolus a
513	160	5.8	356	2	Q6X3X9	Q6x3x9	ipomoea tri
514	160	5.8	361	2	Q6X3Y0	Q6x3y0	ipomoea hed
515	160	5.8	383	2	Q9LRE4	Q9lre4	ipomoea bat
516	160	5.8	432	2	Q7N614	Q7n614	photorhabdu
517	160	5.8	480	2	Q6F4D6	Q6f4d6	catharanthu
518	159.5	5.8	277	2	Q7XFQ3	Q7xfq3	oryza sativ
519	159.5	5.8	286	2	Q8S657	Q8s657	oryza sativ
520	159.5	5.8	286	2	Q7XFW0	Q7xfw0	oryza sativ
521	159.5	5.8	392	2	Q737I4	Q737i4	bacillus ce
522	159.5	5.8	404	2	Q6W222	Q6w222	rhizobium s
523	159.5	5.8	467	2	Q8LC96	Q8lc96	arabidopsis
524	159.5	5.8	469	2	Q69IV0	Q69iv0	oryza sativ
525	159.5	5.8	478	2	O23382	O23382	arabidopsis
526	159	5.7	285	2	Q8TOU7	Q8t0u7	drosophila
527	159	5.7	287	1	UFO7_MANES	Q40289	manihot esc
528	159	5.7	445	2	Q69TH5	Q69th5	oryza sativ

529	159	5.7	460	2	Q9LFJ8	Q9lfj8	arabidopsis
530	159	5.7	474	2	Q942B6	Q942b6	oryza sativ
531	158.5	5.7	156	2	Q96DH9	Q96dh9	homo sapien
532	158.5	5.7	470	1	HQGT_RAUSE	Q9ar73	rauvolfia s
533	158.5	5.7	471	1	UFO2_MAIZE	P16165	zea mays (m
534	158.5	5.7	471	2	Q8W1D2	Q8w1d2	zea mays (m
535	158.5	5.7	473	2	Q94IP3	Q94ip3	solanum sog
536	158.5	5.7	490	2	Q6Z473	Q6z473	oryza sativ
537	158	5.7	301	2	Q705T5	Q705t5	arabidopsis
538	158	5.7	485	2	Q7X709	Q7x709	oryza sativ
539	158	5.7	487	2	Q7XJ51	Q7xj51	allium cepa
540	158	5.7	491	2	Q7XV42	Q7xv42	oryza sativ
541	158	5.7	496	2	Q9ZQ97	Q9zq97	arabidopsis
542	157.5	5.7	435	2	Q9CD88	Q9cd88	mycobacteri
543	157.5	5.7	467	2	O82385	O82385	arabidopsis
544	157.5	5.7	471	1	UFO3_MAIZE	P16167	zea mays (m
545	157.5	5.7	471	2	Q8GSG7	Q8gsg7	zea mays (m
546	157.5	5.7	504	2	Q851J7	Q851j7	oryza sativ
547	157.5	5.7	535	2	Q7XKK4	Q7xkk4	oryza sativ
548	157	5.7	317	2	O16510	O16510	caenorhabdi
549	157	5.7	461	2	Q9XC67	Q9xc67	streptomyce
550	157	5.7	486	2	Q6Z689	Q6z689	oryza sativ
551	157	5.7	496	2	Q7XKI0	Q7xki0	oryza sativ
552	156.5	5.7	442	2	O81010	O81010	arabidopsis
553	156.5	5.7	463	2	Q8S997	Q8s997	phaseolus a
554	156.5	5.7	490	2	Q7XW22	Q7xw22	oryza sativ
555	156.5	5.7	503	2	Q7F9N6	Q7f9n6	oryza sativ
556	156	5.6	406	2	Q97TQ3	Q97tq3	clostridium
557	156	5.6	466	2	Q7XT97	Q7xt97	oryza sativ
558	156	5.6	473	2	Q9LSY9	Q9lsy9	arabidopsis
559	156	5.6	479	2	Q942C5	Q942c5	oryza sativ
560	155.5	5.6	392	2	O34539	O34539	bacillus su
561	155.5	5.6	464	2	Q8W2B6	Q8w2b6	zea mays (m
562	155.5	5.6	496	2	Q8RX23	Q8rx23	arabidopsis
563	155.5	5.6	496	2	Q9LVF0	Q9lvf0	arabidopsis
564	155	5.6	301	2	Q705S7	Q705s7	arabidopsis
565	155	5.6	470	2	Q9ZQ54	Q9zq54	arabidopsis
566	154.5	5.6	431	2	Q47843	Q47843	pantoea agg
567	154.5	5.6	478	2	Q942B8	Q942b8	oryza sativ
568	154.5	5.6	485	2	Q8S999	Q8s999	phaseolus a
569	154.5	5.6	492	2	Q8S7R8	Q8s7r8	oryza sativ
570	154	5.6	362	2	Q6X3X1	Q6x3x1	ipomoea alb
571	154	5.6	421	2	Q8KHE4	Q8khe4	nocardia ae
572	154	5.6	452	2	Q8GVE3	Q8gve3	citrus maxi
573	154	5.6	495	2	Q9ZQ94	Q9zq94	arabidopsis
574	153.5	5.5	301	2	Q705R8	Q705r8	arabidopsis
575	153.5	5.5	301	2	Q705T0	Q705t0	arabidopsis
576	153.5	5.5	447	2	Q9C768	Q9c768	arabidopsis
577	153.5	5.5	469	2	Q9LR44	Q9lr44	arabidopsis
578	153.5	5.5	478	2	Q8LED6	Q8led6	arabidopsis
579	153.5	5.5	478	2	Q65XD0	Q65xd0	oryza sativ
580	153.5	5.5	487	1	UFO5_MANES	Q40287	manihot esc
581	153.5	5.5	487	2	Q6Z485	Q6z485	oryza sativ
582	153	5.5	451	2	Q9SNB1	Q9snb1	arabidopsis
583	153	5.5	490	2	Q6I5X0	Q6i5x0	oryza sativ
584	153	5.5	496	2	Q9ZQ96	Q9zq96	arabidopsis
585	152.5	5.5	301	2	Q705R7	Q705r7	arabidopsis

586	152.5	5.5	329	2	Q7XWK6	Q7xwk6	oryza sativ
587	152.5	5.5	401	2	Q8KNC3	Q8knc3	micromonosp
588	152.5	5.5	459	2	Q8LKT5	Q8lkt5	sorghum bic
589	152.5	5.5	469	2	Q69UF5	Q69uf5	oryza sativ
590	152.5	5.5	470	2	Q9ASY6	Q9asy6	arabidopsis
591	152.5	5.5	495	2	Q8GYL0	Q8gyl0	arabidopsis
592	152.5	5.5	495	2	Q9ZQ95	Q9zq95	arabidopsis
593	152	5.5	472	2	Q65X83	Q65x83	oryza sativ
594	152	5.5	495	2	Q7SFJ4	Q7sfj4	neurospora
595	151.5	5.5	301	2	Q705S0	Q705s0	arabidopsis
596	151.5	5.5	301	2	Q705S9	Q705s9	arabidopsis
597	151.5	5.5	438	2	Q9CD91	Q9cd91	mycobacteri
598	151.5	5.5	450	2	Q9FI96	Q9fi96	arabidopsis
599	151.5	5.5	478	2	Q9ZVX4	Q9zvx4	arabidopsis
600	151.5	5.5	497	2	Q9FYU7	Q9fyu7	brassica na
601	151.5	5.5	519	2	Q6H7J1	Q6h7j1	oryza sativ
602	151	5.5	451	2	Q8LFF5	Q8lff5	arabidopsis
603	151	5.5	451	2	Q9FI98	Q9fi98	arabidopsis
604	151	5.5	453	2	Q9S9P6	Q9s9p6	arabidopsis
605	151	5.5	457	2	Q8LKT2	Q8lkt2	sorghum bic
606	151	5.5	470	2	Q940V3	Q940v3	arabidopsis
607	151	5.5	489	2	Q9M9E7	Q9m9e7	arabidopsis
608	150.5	5.4	301	2	Q705R9	Q705r9	arabidopsis
609	150.5	5.4	301	2	Q705S1	Q705s1	arabidopsis
610	150.5	5.4	301	2	Q705S2	Q705s2	arabidopsis
611	150.5	5.4	301	2	Q705S3	Q705s3	arabidopsis
612	150.5	5.4	423	2	Q7NEX1	Q7nex1	gloeobacter
613	150	5.4	478	2	Q8W3P8	Q8w3p8	phaseolus a
614	149.5	5.4	449	2	P95130	P95130	mycobacteri
615	149.5	5.4	449	2	Q7TXJ4	Q7txj4	mycobacteri
616	149.5	5.4	461	2	Q6VAA7	Q6vaa7	stevia reba
617	149.5	5.4	466	2	Q43526	Q43526	lycopersico
618	149.5	5.4	470	2	Q7XWK2	Q7xwk2	oryza sativ
619	149.5	5.4	487	2	Q6F4D5	Q6f4d5	catharanthu
620	149.5	5.4	489	2	Q9SK82	Q9sk82	arabidopsis
621	149.5	5.4	1574	2	Q6BN88	Q6bn88	debaryomyce
622	149	5.4	392	2	Q6HI79	Q6hi79	bacillus th
623	149	5.4	507	2	Q9SCP6	Q9scp6	arabidopsis
624	149	5.4	520	2	Q6AT17	Q6at17	oryza sativ
625	148.5	5.4	301	2	Q705R4	Q705r4	arabidopsis
626	148.5	5.4	301	2	Q705U2	Q705u2	arabidopsis
627	148.5	5.4	347	2	Q8L5C7	Q8l5c7	pisum sativ
628	148.5	5.4	412	2	Q9S0P6	Q9s0p6	streptomyce
629	148.5	5.4	417	2	Q84WC5	Q84wc5	arabidopsis
630	148.5	5.4	438	2	Q9SNB3	Q9snb3	arabidopsis
631	148.5	5.4	464	2	Q9FI99	Q9fi99	arabidopsis
632	148.5	5.4	472	2	Q65X84	Q65x84	oryza sativ
633	148.5	5.4	485	2	Q9LSY8	Q9lsy8	arabidopsis
634	148	5.3	474	2	Q6Z478	Q6z478	oryza sativ
635	148	5.3	485	2	Q84ZE4	Q84ze4	oryza sativ
636	148	5.3	559	2	Q8S996	Q8s996	phaseolus a
637	147.5	5.3	301	2	Q705R3	Q705r3	arabidopsis
638	147.5	5.3	301	2	Q705U1	Q705u1	arabidopsis
639	147.5	5.3	442	2	Q9M0P3	Q9m0p3	arabidopsis
640	147.5	5.3	455	2	Q9ZVY5	Q9zvy5	arabidopsis
641	147.5	5.3	460	2	Q9AUV2	Q9auv2	oryza sativ
642	147.5	5.3	466	2	Q9LSM0	Q9lsm0	arabidopsis

643	147.5	5.3	474	2	O04930	O04930	arabidopsis
644	147.5	5.3	479	2	Q9LMF0.	Q9lmf0	arabidopsis
645	147.5	5.3	480	2	Q9LSY4	Q9lsy4	arabidopsis
646	147.5	5.3	481	2	O82381	O82381	arabidopsis
647	147	5.3	453	2	Q8LAI9	Q8lai9	arabidopsis
648	147	5.3	495	2	Q6ESW8	Q6esw8	oryza sativ
649	146.5	5.3	301	2	Q705T4	Q705t4	arabidopsis
650	146.5	5.3	301	2	Q705T9	Q705t9	arabidopsis
651	146.5	5.3	418	2	Q93Z19	Q93z19	arabidopsis
652	146.5	5.3	424	2	Q6VAB1	Q6vab1	stevia reba
653	146.5	5.3	447	2	Q8GWA0	Q8gwa0	arabidopsis
654	146.5	5.3	452	2	Q9STE3	Q9ste3	arabidopsis
655	146.5	5.3	458	2	O23406	O23406	arabidopsis
656	146.5	5.3	461	2	Q6ER38	Q6er38	oryza sativ
657	146.5	5.3	466	2	Q8GX09	Q8gx09	arabidopsis
658	146.5	5.3	476	2	P93364	P93364	nicotiana t
659	146.5	5.3	476	2	Q9AT53	Q9at53	nicotiana t
660	146.5	5.3	496	2	Q9ZQ98	Q9zq98	arabidopsis
661	146.5	5.3	504	2	Q6K2W8	Q6k2w8	oryza sativ
662	146	5.3	359	2	Q8GYB0	Q8gyb0	arabidopsis
663	146	5.3	452	2	O23380	O23380	arabidopsis
664	146	5.3	475	2	Q6WFW1	Q6wfw1	crocus sati
665	146	5.3	480	2	Q9FTW7	Q9ftw7	oryza sativ
666	146	5.3	481	2	Q7XI35	Q7xi35	oryza sativ
667	146	5.3	491	2	Q9ZQ99	Q9zq99	arabidopsis
668	146	5.3	772	2	Q75I83	Q75i83	oryza sativ
669	145.5	5.3	301	2	Q705T6	Q705t6	arabidopsis
670	145.5	5.3	481	2	Q9LNI1	Q9lni1	arabidopsis
671	145	5.2	274	2	Q8S9A2	Q8s9a2	phaseolus a
672	145	5.2	428	2	Q6ZHS1	Q6zhs1	oryza sativ
673	145	5.2	453	2	O22186	O22186	arabidopsis
674	145	5.2	468	2	Q69IU8	Q69iu8	oryza sativ
675	145	5.2	479	2	Q8H3X8	Q8h3x8	oryza sativ
676	145	5.2	480	2	Q6QDB6	Q6qdb6	rhodiola sa
677	145	5.2	494	2	Q6K755	Q6k755	oryza sativ
678	144.5	5.2	446	2	Q6D1R8	Q6dlr8	erwinia car
679	144.5	5.2	481	2	Q8W237	Q8w237	dorotheanth
680	144.5	5.2	510	2	Q8LJZ7	Q8ljz7	sorghum bic
681	144.5	5.2	571	2	Q8GRS8	Q8grs8	oryza sativ
682	144	5.2	392	2	Q63AU6	Q63au6	bacillus ce
683	144	5.2	407	2	Q97FM0	Q97fm0	clostridium
684	144	5.2	454	2	Q69TJ1	Q69tj1	oryza sativ
685	144	5.2	460	2	Q9ZR27	Q9zr27	perilla fru
686	144	5.2	468	2	Q6VAA5	Q6vaa5	stevia reba
687	144	5.2	479	2	Q6VAB3	Q6vab3	stevia reba
688	144	5.2	481	2	Q8W4G1	Q8w4g1	arabidopsis
689	144	5.2	498	2	Q6ESW3	Q6esw3	oryza sativ
690	143.5	5.2	287	2	Q8L6L3	Q8l6l3	hordeum vul
691	143.5	5.2	451	2	Q8RXA4	Q8rxa4	lycopersico
692	143.5	5.2	462	2	Q94BM9	Q94bm9	arabidopsis
693	143.5	5.2	479	2	Q9LML6	Q9lml6	arabidopsis
694	143.5	5.2	485	2	Q8S9A7	Q8s9a7	phaseolus a
695	143.5	5.2	493	2	Q69XD3	Q69xd3	oryza sativ
696	143.5	5.2	502	2	Q67W01	Q67w01	oryza sativ
697	143.5	5.2	524	2	Q9LGG2	Q9lgg2	oryza sativ
698	143	5.2	453	2	Q9FN26	Q9fn26	arabidopsis
699	143	5.2	462	2	Q8L9U9	Q8l9u9	arabidopsis

700	143	5.2	469	2	Q9LNI4	Q9lni4	arabidopsis
701	143	5.2	480	2	Q8W4C2	Q8w4c2	arabidopsis
702	143	5.2	481	2	Q9ZWJ3	Q9zwj3	arabidopsis
703	142.5	5.1	414	2	Q9S595	Q9s595	nocardia ae
704	142.5	5.1	452	2	Q8GZ65	Q8gz65	arabidopsis
705	142.5	5.1	468	2	Q681W3	Q681w3	arabidopsis
706	142.5	5.1	476	2	Q9AT54	Q9at54	nicotiana t
707	142.5	5.1	477	2	Q6Z035	Q6z035	oryza sativ
708	142.5	5.1	477	2	Q6ZF65	Q6zf65	oryza sativ
709	142.5	5.1	1307	2	Q6C8M8	Q6c8m8	yarrowia li
710	142	5.1	424	2	O68841	O68841	streptomyce
711	142	5.1	482	2	Q8H0F2	Q8h0f2	gentiana tr
712	141.5	5.1	333	2	Q81CW9	Q81cw9	bacillus ce
713	141.5	5.1	449	2	Q9SNB0	Q9snb0	arabidopsis
714	141.5	5.1	476	2	P93365	P93365	nicotiana t
715	141.5	5.1	489	2	Q9SMG6	Q9smg6	dorotheanth
716	141.5	5.1	492	2	Q7XSZ0	Q7xsz0	oryza sativ
717	141	5.1	149	2	Q99912	Q99912	homo sapien
718	141	5.1	394	1	UFO6 MANES	Q40288	manihot esc
719	141	5.1	462	2	Q9LK73	Q9lk73	arabidopsis
720	141	5.1	472	2	Q75I86	Q75i86	oryza sativ
721	141	5.1	480	2	Q65X86	Q65x86	oryza sativ
722	141	5.1	481	2	O81498	O81498	arabidopsis
723	141	5.1	482	2	Q65YR5	Q65yr5	gentiana sc
724	141	5.1	515	2	Q69KM1	Q69km1	oryza sativ
725	140.5	5.1	346	1	UFO2 MANES	Q40285	manihot esc
726	140.5	5.1	449	2	Q9LTH2	Q9lth2	arabidopsis
727	140.5	5.1	459	2	Q8W2B7	Q8w2b7	zea mays (m
728	140.5	5.1	463	2	Q767C8	Q767c8	iris hollan
729	140.5	5.1	486	2	Q9LEQ4	Q9leq4	arabidopsis
730	140.5	5.1	507	2	Q9FTW1	Q9ftw1	oryza sativ
731	140	5.1	478	2	Q8H0F1	Q8h0f1	torenia hyb
732	140	5.1	480	2	Q9FE68	Q9fe68	arabidopsis
733	140	5.1	515	2	Q69JV3	Q69jv3	oryza sativ
734	139.5	5.0	227	2	Q9CAY9	Q9cay9	arabidopsis
735	139.5	5.0	241	1	UFO4 MANES	Q40286	manihot esc
736	139.5	5.0	379	2	Q93HI3	Q93hi3	streptomyce
737	139.5	5.0	397	2	Q825U1	Q825u1	streptomyce
738	139.5	5.0	431	2	Q6YY41	Q6yy41	oryza sativ
739	139.5	5.0	452	2	Q9XIQ4	Q9xiq4	arabidopsis
740	139.5	5.0	481	2	Q9LVR1	Q9lvr1	arabidopsis
741	139	5.0	98	2	Q645Q1	Q645q1	fundulus he
742	139	5.0	461	2	Q67XH7	Q67xh7	arabidopsis
743	139	5.0	461	2	Q9LHJ2	Q9lhj2	arabidopsis
744	139	5.0	464	2	Q9SGA8	Q9sga8	arabidopsis
745	139	5.0	467	2	Q9SY84	Q9sy84	arabidopsis
746	139	5.0	474	2	Q8H462	Q8h462	oryza sativ
747	139	5.0	492	2	Q9SBL1	Q9sbl1	sorghum bic
748	138.5	5.0	438	2	Q9M3H8	Q9m3h8	cicer ariet
749	138.5	5.0	444	2	Q9ZU71	Q9zu71	arabidopsis
750	138.5	5.0	446	2	Q8RU65	Q8ru65	oryza sativ
751	138.5	5.0	449	1	UFO1 MANES	Q40284	manihot esc
752	138.5	5.0	450	2	Q8LAE5	Q8lae5	arabidopsis
753	138.5	5.0	450	2	Q9LME9	Q9lme9	arabidopsis
754	138.5	5.0	460	2	Q9M052	Q9m052	arabidopsis
755	138	5.0	154	1	UFOG_VITVI	P51094	vitis vinif
756	138	5.0	381	2	Q9ZWQ3	Q9zwq3	vigna mungo

757	138	5.0	385	2	Q9STE4	Q9ste4	arabidopsis
758	138	5.0	438	2	O22183	O22183	arabidopsis
759	138	5.0	455	2	O64733	O64733	arabidopsis
760	138	5.0	458	2	Q6VAB4	Q6vab4	stevia reba
761	138	5.0	476	2	Q6AVQ5	Q6avq5	oryza sativ
762	138	5.0	478	2	Q6Z6F0	Q6z6f0	oryza sativ
763	138	5.0	482	2	Q65YR6	Q65yr6	gentiana sc
764	138	5.0	497	2	Q7XTG5	Q7xtg5	oryza sativ
765	138	5.0	501	2	Q67TS1	Q67ts1	oryza sativ
766	138	5.0	503	2	Q7XE18	Q7xe18	oryza sativ
767	137.5	5.0	431	2	Q8GCS3	Q8gcs3	pantoea ste
768	137.5	5.0	443	2	Q9ZR26	Q9zr26	perilla fru
769	137.5	5.0	463	2	Q6ZBR2	Q6zbr2	oryza sativ
770	137.5	5.0	467	2	P93709	P93709	nicotiana t
771	137.5	5.0	501	2	Q6K2Q2	Q6k2q2	oryza sativ
772	137.5	5.0	512	2	Q6Z381	Q6z381	oryza sativ
773	137	4.9	476	2	Q9SXF2	Q9sxf2	scutellaria
774	137	4.9	491	2	Q94CZ1	Q94cz1	oryza sativ
775	136.5	4.9	396	2	Q70J67	Q70j67	streptomyce
776	136.5	4.9	488	2	P93789	P93789	solanum tub
777	136	4.9	215	2	Q9HCT7	Q9hct7	homo sapien
778	136	4.9	345	2	Q84RI3	Q84ri3	beta vulgar
779	136	4.9	452	2	P95747	P95747	streptomyce
780	136	4.9	465	2	Q65XC9	Q65xc9	oryza sativ
781	136	4.9	471	2	Q942B3	Q942b3	oryza sativ
782	136	4.9	489	2	Q6ESV8	Q6esv8	oryza sativ
783	135.5	4.9	380	2	Q8GWE5	Q8gwe5	arabidopsis
784	135.5	4.9	453	2	Q65X85	Q65x85	oryza sativ
785	135.5	4.9	478	2	Q8H3V2	Q8h3v2	oryza sativ
786	135	4.9	267	2	Q8RWA6	Q8rwa6	arabidopsis
787	135	4.9	470	2	Q9ZU72	Q9zu72	arabidopsis
788	135	4.9	474	2	Q6VAB2	Q6vab2	stevia reba
789	135	4.9	490	2	Q9SCP5	Q9scp5	arabidopsis
790	135	4.9	523	2	Q8S9A1	Q8s9a1	phaseolus a
791	134.5	4.9	305	2	O52939	O52939	calothrix v
792	134.5	4.9	387	2	Q81Q01	Q81q01	bacillus an
793	134.5	4.9	392	2	Q6HY70	Q6hy70	bacillus an
794	134.5	4.9	441	2	Q76MR7	Q76mr7	scutellaria
795	134.5	4.9	447	2	Q9FN28	Q9fn28	arabidopsis
796	134	4.8	174	2	Q9NF29	Q9nf29	caenorhabdi
797	134	4.8	419	2	Q76KZ6	Q76kz6	streptomyce
798	134	4.8	446	2	Q8LAB5	Q8lab5	arabidopsis
799	134	4.8	455	2	Q9T080	Q9t080	arabidopsis
800	134	4.8	456	2	O23270	O23270	arabidopsis
801	134	4.8	466	2	Q8RY86	Q8ry86	arabidopsis
802	134	4.8	510	2	Q943K5	Q943k5	oryza sativ
803	133.5	4.8	398	2	Q97HL4	Q97hl4	clostridium
804	133.5	4.8	462	2	Q9AUU9	Q9auu9	oryza sativ
805	133.5	4.8	479	2	Q7XJ50	Q7xj50	allium cepa
806	133.5	4.8	496	2	Q94CY6	Q94cy6	oryza sativ
807	133	4.8	365	2	Q8GZ08	Q8gz08	arabidopsis
808	133	4.8	470	2	Q8S342	Q8s342	capsicum an
809	133	4.8	481	2	Q6VAB0	Q6vab0	stevia reba
810	132.5	4.8	447	2	Q9STE6	Q9ste6	arabidopsis
811	132.5	4.8	447	2	Q9XIQ5	Q9xiq5	arabidopsis
812	132.5	4.8	485	2	Q69X83	Q69x83	oryza sativ
813	132.5	4.8	495	2	Q6VAA9	Q6vaa9	stevia reba

814	132	4.8	497	2	Q6ZBE1	Q6zbe1	oryza sativ
815	131.5	4.8	287	2	Q7BV94	Q7bv94	bacillus su
816	131.5	4.8	346	2	Q8W1D9	Q8wld9	jatropha cu
817	131.5	4.8	392	2	Q8KNF2	Q8knf2	micromonosp
818	130.5	4.7	170	2	Q9LMF1	Q9lmf1	arabidopsis
819	130.5	4.7	389	2	Q83X61	Q83x61	streptomyce
820	130.5	4.7	453	2	Q9LTH3	Q9lth3	arabidopsis
821	130.5	4.7	478	2	Q66PF2	Q66pf2	fragaria an
822	130	4.7	455	1	UFOG_HORVU	P14726	hordeum vul
823	130	4.7	460	2	Q9LTA3	Q9lta3	arabidopsis
824	130	4.7	490	2	Q6L4T2	Q6l4t2	oryza sativ
825	129.5	4.7	379	2	Q67G38	Q67g38	streptomyce
826	129.5	4.7	400	2	Q97HK4	Q97hk4	clostridium
827	129.5	4.7	466	2	Q6JAH0	Q6jah0	sorghum bic
828	129.5	4.7	472	2	Q8LEG2	Q8leg2	arabidopsis
829	129.5	4.7	487	2	Q69JV0	Q69jv0	oryza sativ
830	129.5	4.7	1227	2	Q751Z4	Q751z4	ashbya goss
831	129	4.7	414	2	Q8S9A3	Q8s9a3	phaseolus a
832	129	4.7	470	2	Q8LR92	Q8lr92	oryza sativ
833	128.5	4.6	394	1	YC55_METJA	Q58652	methanococc
834	128.5	4.6	396	2	Q939Q6	Q939q6	streptomyce
835	128.5	4.6	430	1	OLED_STRAT	Q53685	streptomyce
836	128.5	4.6	453	2	Q9LS21	Q9ls21	arabidopsis
837	128.5	4.6	469	2	Q7XJ49	Q7xj49	allium cepa
838	128	4.6	309	2	Q94BU0	Q94bu0	arabidopsis
839	128	4.6	461	2	Q7NHR8	Q7nhr8	gloeobacter
840	128	4.6	462	2	Q6JAG7	Q6jag7	sorghum bic
841	127.5	4.6	470	2	Q852C2	Q852c2	oryza sativ
842	127.5	4.6	473	2	Q8LJC6	Q8ljc6	oryza sativ
843	127.5	4.6	474	2	Q7F0B2	Q7f0b2	oryza sativ
844	127.5	4.6	482	2	Q8RU72	Q8ru72	nicotiana t
845	127.5	4.6	493	2	Q7XKG0	Q7xkg0	oryza sativ
846	127.5	4.6	1209	2	Q6CUV2	Q6cuv2	kluveromyc
847	127	4.6	463	2	Q8RXA5	Q8rxa5	zea mays (m
848	127	4.6	470	2	Q9AUV1	Q9auv1	oryza sativ
849	127	4.6	488	2	Q8VZE9	Q8vze9	arabidopsis
850	127	4.6	528	2	Q8LNA9	Q8lna9	oryza sativ
851	126.5	4.6	356	2	Q7S0K9	Q7s0k9	neurospora
852	126.5	4.6	486	2	Q6AUW7	Q6auw7	oryza sativ
853	126	4.6	440	2	O64732	O64732	arabidopsis
854	126	4.6	444	2	Q8S9A5	Q8s9a5	phaseolus a
855	126	4.6	484	2	Q6AUW6	Q6auw6	oryza sativ
856	126	4.6	508	2	Q6H8F6	Q6h8f6	oryza sativ
857	125.5	4.5	175	2	Q6H8F9	Q6h8f9	oryza sativ
858	125.5	4.5	381	2	O05496	O05496	bacillus su
859	125.5	4.5	461	2	Q93ZG5	Q93zg5	arabidopsis
860	125.5	4.5	487	2	Q7XSY7	Q7xsy7	oryza sativ
861	125	4.5	463	2	Q7XU02	Q7xu02	oryza sativ
862	124.5	4.5	504	2	Q95GQ5	Q95gq5	nepenthes s
863	124	4.5	358	2	Q7XKM2	Q7xkm2	oryza sativ
864	123.5	4.5	464	2	Q7XQJ5	Q7xqj5	oryza sativ
865	123.5	4.5	475	2	Q7XMA8	Q7xma8	oryza sativ
866	123.5	4.5	482	2	Q6Z4C0	Q6z4c0	oryza sativ
867	123.5	4.5	490	2	Q6JAG5	Q6jag5	sorghum bic
868	123	4.4	464	2	Q7XQJ9	Q7xqj9	oryza sativ
869	123	4.4	465	2	Q8S465	Q8s465	zea mays (m
870	123	4.4	467	2	Q93XP7	Q93xp7	zea mays (m

871	123	4.4	469	2	Q7XMQ0	Q7xmQ0	oryza sativ
872	123	4.4	637	2	Q8S1P6	Q8slp6	oryza sativ
873	122.5	4.4	455	2	Q9FI97	Q9fi97	arabidopsis
874	122.5	4.4	487	2	Q75HA1	Q75ha1	oryza sativ
875	122.5	4.4	493	2	Q84M46	Q84m46	oryza sativ
876	122.5	4.4	1211	2	Q9Y751	Q9y751	pichia past
877	122.5	4.4	2259	1	YCF2_PHYPA	P61243	physcomitre
878	122	4.4	135	2	Q50456	Q50456	mycobacteri
879	122	4.4	388	2	Q9RPA1	Q9rpal	streptomyce
880	122	4.4	464	2	Q6JAG9	Q6jag9	sorghum bic
881	122	4.4	501	2	Q9FU68	Q9fu68	oryza sativ
882	122	4.4	1310	2	Q7RZT3	Q7rzt3	neurospora
883	121.5	4.4	485	2	Q6Z4B7	Q6z4b7	oryza sativ
884	121	4.4	482	2	Q7XZD0	Q7xzd0	glycyrrhiza
885	120.5	4.4	422	2	Q9F826	Q9f826	micromonosp
886	120.5	4.4	490	2	Q9SJL0	Q9sjl0	arabidopsis
887	120.5	4.4	491	2	Q67TS4	Q67ts4	oryza sativ
888	120.5	4.4	497	2	Q69X81	Q69x81	oryza sativ
889	120.5	4.4	498	2	Q9FU69	Q9fu69	oryza sativ
890	120	4.3	418	2	Q9RYI3	Q9ryi3	deinococcus
891	119.5	4.3	200	2	Q6AT14	Q6at14	oryza sativ
892	119.5	4.3	270	2	Q6AUW5	Q6auw5	oryza sativ
893	119.5	4.3	422	2	O70023	O70023	streptomyce
894	119.5	4.3	448	2	Q9LJA6	Q9lja6	arabidopsis
895	119.5	4.3	504	2	Q94NR5	Q94nr5	nepenthes b
896	119.5	4.3	504	2	Q95GS1	Q95gs1	nepenthes c
897	119.5	4.3	504	2	Q95GT1	Q95gt1	nepenthes v
898	119.5	4.3	504	2	Q7IGS0	Q7igs0	nepenthes m
899	119.5	4.3	721	2	Q6BHK6	Q6bhk6	debaryomyce
900	119	4.3	194	2	Q8GSR1	Q8gsr1	triticum ae
901	119	4.3	194	2	Q8GSR3	Q8gsr3	triticum ae
902	119	4.3	196	2	Q8GSR2	Q8gsr2	triticum ae
903	119	4.3	483	2	Q75HJ2	Q75hj2	oryza sativ
904	118.5	4.3	418	1	MGT_STRLI	Q54387	streptomyce
905	118.5	4.3	418	2	Q9ADH3	Q9adh3	streptomyce
906	118.5	4.3	453	2	Q9T081	Q9t081	arabidopsis
907	118.5	4.3	463	2	Q7XU03	Q7xu03	oryza sativ
908	118.5	4.3	497	2	Q9FU67	Q9fu67	oryza sativ
909	118.5	4.3	504	2	Q95GU2	Q95gu2	nepenthes i
910	118.5	4.3	679	2	Q8J1H4	Q8jlh4	ustilago ma
911	118	4.3	464	2	Q6JAG8	Q6jag8	sorghum bic
912	118	4.3	468	2	Q9LVW3	Q9lvw3	arabidopsis
913	118	4.3	507	2	Q6Z4L0	Q6z4l0	oryza sativ
914	118	4.3	698	2	Q95AS6	Q95as6	pseudophoen
915	117.5	4.2	436	2	Q76GS1	Q76gs1	nepenthes v
916	117	4.2	256	2	Q7PJA1	Q7pja1	anopheles g
917	117	4.2	460	2	Q7WTE9	Q7wte9	streptomyce
918	117	4.2	481	2	Q8W491	Q8w491	arabidopsis
919	117	4.2	497	2	Q67TS2	Q67ts2	oryza sativ
920	116.5	4.2	419	2	Q6U868	Q6u868	mycobacteri
921	116.5	4.2	419	2	Q6U870	Q6u870	mycobacteri
922	116.5	4.2	428	2	O69000	O69000	mycobacteri
923	116.5	4.2	472	2	Q9FSS3	Q9fss3	oryza sativ
924	116.5	4.2	504	2	Q95GQ1	Q95gq1	nepenthes g
925	116.5	4.2	504	2	Q95GU1	Q95gu1	nepenthes i
926	116	4.2	169	2	Q8L7D4	Q8l7d4	arabidopsis
927	116	4.2	488	2	Q6ZBR9	Q6zbr9	oryza sativ

928	115.5	4.2	401	2	Q9ZGB4	Q9zgb4	streptomyce
929	115.5	4.2	433	2	Q9SYC4	Q9syc4	arabidopsis
930	115.5	4.2	502	2	Q7XKG1	Q7xkg1	oryza sativ
931	115.5	4.2	504	2	Q95GS9	Q95gs9	nepenthes m
932	115.5	4.2	504	2	Q95GT0	Q95gt0	nepenthes t
933	115.5	4.2	504	2	Q95GU3	Q95gu3	nepenthes r
934	115.5	4.2	1553	2	Q7S1I0	Q7s1i0	neurospora
935	115	4.2	390	2	Q9ZGB8	Q9zgb8	streptomyce
936	115	4.2	483	2	Q94C57	Q94c57	arabidopsis
937	115	4.2	615	2	Q9XIG1	Q9xig1	arabidopsis
938	115	4.2	1516	2	Q9Y752	Q9y752	candida alb
939	114.5	4.1	361	2	Q6M068	Q6m068	methanococc
940	114.5	4.1	417	2	Q9ZGB1	Q9zgb1	streptomyce
941	114.5	4.1	494	2	Q7XVP1	Q7xvp1	oryza sativ
942	114.5	4.1	504	2	Q94NV9	Q94nv9	nepenthes r
943	114.5	4.1	504	2	Q95GP2	Q95gp2	nepenthes s
944	114.5	4.1	504	2	Q95GR1	Q95gr1	nepenthes d
945	114.5	4.1	504	2	Q95GR4	Q95gr4	nepenthes m
946	114.5	4.1	504	2	Q95GR5	Q95gr5	nepenthes p
947	114.5	4.1	504	2	Q95GT3	Q95gt3	nepenthes t
948	114.5	4.1	504	2	Q95GT4	Q95gt4	nepenthes h
949	114.5	4.1	504	2	Q7IGS1	Q7igs1	nepenthes a
950	114	4.1	425	2	Q83X73	Q83x73	streptomyce
951	114	4.1	698	2	Q95AS0	Q95as0	orania tris
952	113.5	4.1	402	2	Q9F8U7	Q9f8u7	streptomyce
953	113.5	4.1	426	2	O87831	O87831	streptomyce
954	113.5	4.1	460	2	Q9ZQG3	Q9zqg3	arabidopsis
955	113.5	4.1	473	1	UFOG_PETHY	Q43716	petunia hyb
956	113.5	4.1	484	2	Q7Y232	Q7y232	arabidopsis
957	113.5	4.1	504	2	Q95GT5	Q95gt5	nepenthes a
958	113	4.1	380	2	Q67G44	Q67g44	streptomyce
959	113	4.1	415	2	O33939	O33939	saccharopol
960	113	4.1	417	2	O86304	O86304	streptomyce
961	113	4.1	463	2	Q6PVW5	Q6pvw5	fragaria an
962	113	4.1	478	2	O49492	O49492	arabidopsis
963	113	4.1	732	2	Q95D43	Q95d43	magnolia do
964	113	4.1	732	2	Q95D67	Q95d67	michelia hy
965	112.5	4.1	281	2	Q18872	Q18872	caenorhabdi
966	112.5	4.1	379	1	YG36_METMA	Q8pwf3	methanosarc
967	112.5	4.1	390	2	Q8GHC2	Q8ghc2	streptomyce
968	112.5	4.1	419	2	Q6U848	Q6u848	mycobacteri
969	112.5	4.1	504	2	Q95GP7	Q95gp7	nepenthes t
970	112.5	4.1	504	2	Q95GQ2	Q95gq2	nepenthes d
971	112.5	4.1	504	2	Q95GS5	Q95gs5	nepenthes t
972	112.5	4.1	555	2	Q93ZJ2	Q93zj2	arabidopsis
973	112.5	4.1	563	2	Q7MAS9	Q7mas9	wolinella...s
974	112.5	4.1	637	2	O23649	O23649	arabidopsis
975	112.5	4.1	637	2	Q9M8Z7	Q9m8z7	arabidopsis
976	112.5	4.1	698	2	Q9TL88	Q9tl88	codonopsis
977	112.5	4.1	732	2	O98710	O98710	pinckneya p
978	112.5	4.1	732	2	Q9TJQ2	Q9tjq2	rustia sple
979	112.5	4.1	732	2	Q9TJY8	Q9tjy8	condaminea
980	112	4.0	431	2	Q9MS86	Q9ms86	magnolia st
981	112	4.0	684	2	Q7YM49	Q7ym49	liriodendro
982	112	4.0	684	2	Q7YM51	Q7ym51	eupomatia b
983	112	4.0	698	2	Q95AT8	Q95at8	caryota mit
984	112	4.0	732	2	Q95D22	Q95d22	magnolia sc

985	112	4.0	732	2	Q95D87	Q95d87	magnolia	ko
986	112	4.0	732	2	Q95DA1	Q95da1	magnolia	gr
987	111.5	4.0	267	2	Q7VFR3	Q7vfr3	helicobacte	
988	111.5	4.0	374	2	Q8X5L5	Q8x5l5	escherichia	
989	111.5	4.0	465	2	Q9LZD8	Q9lzd8	arabidopsis	
990	111.5	4.0	504	2	Q94PH2	Q94ph2	nepenthes	r
991	111.5	4.0	504	2	Q94Q55	Q94q55	nepenthes	g
992	111.5	4.0	504	2	Q95GQ8	Q95gq8	nepenthes	m
993	111.5	4.0	504	2	Q95GR6	Q95gr6	nepenthes	r
994	111.5	4.0	504	2	Q95GV2	Q95gv2	nepenthes	d
995	111.5	4.0	504	2	Q95GV5	Q95gv5	nepenthes	a
996	111.5	4.0	504	2	Q7IGR8	Q7igr8	nepenthes	m
997	111.5	4.0	504	2	Q7IGS2	Q7igs2	nepenthes	s
998	111	4.0	403	2	Q8E6C2	Q8e6c2	streptococc	
999	111	4.0	432	2	Q9RN63	Q9rn63	streptomyce	
1000	111	4.0	443	2	P95834	P95834	streptomyce	
1001	111	4.0	504	2	Q95GP6	Q95gp6	nepenthes	m
1002	111	4.0	684	2	Q7YM48	Q7ym48	magnolia	tr
1003	111	4.0	695	2	Q95AS9	Q95as9	chamaedorea	
1004	111	4.0	698	2	Q95AT9	Q95at9	borassus	fl
1005	111	4.0	731	2	Q95D45	Q95d45	liriodendro	
1006	111	4.0	731	2	Q95DB7	Q95db7	magnolia	ma
1007	111	4.0	731	2	Q95DB8	Q95db8	magnolia	ma
1008	111	4.0	731	2	Q95DC0	Q95dc0	magnolia	de
1009	111	4.0	732	2	Q95D23	Q95d23	magnolia	gu
1010	111	4.0	732	2	Q95D24	Q95d24	magnolia	gr
1011	111	4.0	732	2	Q95D26	Q95d26	magnolia	me
1012	111	4.0	732	2	Q95D27	Q95d27	magnolia	ma
1013	111	4.0	732	2	Q95D28	Q95d28	magnolia	le
1014	111	4.0	732	2	Q95D30	Q95d30	magnolia	sp
1015	111	4.0	732	2	Q95D33	Q95d33	magnolia	fr
1016	111	4.0	732	2	Q95D35	Q95d35	magnolia	po
1017	111	4.0	732	2	Q95D59	Q95d59	elmerrillia	
1018	111	4.0	732	2	Q95D60	Q95d60	michelia	fl
1019	111	4.0	732	2	Q95D61	Q95d61	michelia	ba
1020	111	4.0	732	2	Q95D62	Q95d62	michelia	ba
1021	111	4.0	732	2	Q95D63	Q95d63	michelia	od
1022	111	4.0	732	2	Q95D64	Q95d64	michelia	fi
1023	111	4.0	732	2	Q95D65	Q95d65	michelia	ma
1024	111	4.0	732	2	Q95D66	Q95d66	michelia	ch
1025	111	4.0	732	2	Q95D68	Q95d68	michelia	wi
1026	111	4.0	732	2	Q95D69	Q95d69	michelia	ve
1027	111	4.0	732	2	Q95D70	Q95d70	michelia	sh
1028	111	4.0	732	2	Q95D71	Q95d71	michelia	mo
1029	111	4.0	732	2	Q95D72	Q95d72	michelia	ma
1030	111	4.0	732	2	Q95D73	Q95d73	michelia	ma
1031	111	4.0	732	2	Q95D74	Q95d74	michelia	ma
1032	111	4.0	732	2	Q95D75	Q95d75	michelia	la
1033	111	4.0	732	2	Q95D76	Q95d76	michelia	in
1034	111	4.0	732	2	Q95D77	Q95d77	michelia	fo
1035	111	4.0	732	2	Q95D78	Q95d78	michelia	do
1036	111	4.0	732	2	Q95D79	Q95d79	michelia	ch
1037	111	4.0	732	2	Q95D80	Q95d80	michelia	ca
1038	111	4.0	732	2	Q95D85	Q95d85	magnolia	st
1039	111	4.0	732	2	Q95D86	Q95d86	magnolia	sa
1040	111	4.0	732	2	Q95D88	Q95d88	magnolia	bi
1041	111	4.0	732	2	Q95D89	Q95d89	magnolia	ze

1042	111	4.0	732	2	Q95D90	Q95d90	magnolia	sp
1043	111	4.0	732	2	Q95D91	Q95d91	magnolia	sa
1044	111	4.0	732	2	Q95D93	Q95d93	magnolia	da
1045	111	4.0	732	2	Q95D94	Q95d94	magnolia	ca
1046	111	4.0	732	2	Q95D96	Q95d96	magnolia	ca
1047	111	4.0	732	2	Q95D97	Q95d97	magnolia	gi
1048	111	4.0	732	2	Q95DA3	Q95da3	magnolia	pe
1049	111	4.0	732	2	Q95DA8	Q95da8	magnolia	si
1050	111	4.0	732	2	Q95DA9	Q95da9	magnolia	si
1051	111	4.0	732	2	Q95DB0	Q95db0	magnolia	gl
1052	111	4.0	732	2	Q95DB1	Q95db1	kmeria	sept
1053	111	4.0	732	2	Q95DB2	Q95db2	kmeria	dupe
1054	111	4.0	732	2	Q95DB3	Q95db3	magnolia	tr
1055	111	4.0	732	2	Q95DB4	Q95db4	magnolia	ro
1056	111	4.0	732	2	Q95DB5	Q95db5	magnolia	of
1057	111	4.0	732	2	Q95DB6	Q95db6	magnolia	he
1058	111	4.0	732	2	Q95DB9	Q95db9	magnolia	fr
1059	111	4.0	732	2	Q95DC1	Q95dc1	magnolia	pt
1060	111	4.0	732	2	Q95DC2	Q95dc2	magnolia	li
1061	111	4.0	732	2	Q95DC3	Q95dc3	magnolia	he
1062	111	4.0	732	2	Q95DC4	Q95dc4	magnolia	de
1063	111	4.0	732	2	Q95DC5	Q95dc5	magnolia	co
1064	111	4.0	732	2	Q95DC6	Q95dc6	magnolia	ch
1065	111	4.0	842	1	CUL8_YEAST	P47050	saccharomyc	
1066	110.5	4.0	372	2	Q83ZA2	Q83za2	escherichia	
1067	110.5	4.0	406	2	Q93MW2	Q93mw2	nocardia	br
1068	110.5	4.0	445	2	P74079	P74079	synechocyst	
1069	110.5	4.0	503	2	Q95GR2	Q95gr2	nepenthes	h
1070	110.5	4.0	504	2	Q95GR8	Q95gr8	nepenthes	l
1071	110.5	4.0	504	2	Q95GU9	Q95gu9	nepenthes	o
1072	110.5	4.0	504	2	Q95GV6	Q95gv6	nepenthes	b
1073	110.5	4.0	747	2	Q6EW03	Q6ew03	nymphaea	al
1074	110	4.0	300	2	Q7NXT2	Q7nxt2	chromobacte	
1075	110	4.0	379	2	Q9L9F5	Q9l9f5	streptomyce	
1076	110	4.0	416	2	Q6T1C7	Q6tlc7	streptomyce	
1077	110	4.0	448	2	Q8RWP1	Q8rwp1	arabidopsis	
1078	110	4.0	682	2	Q7YM50	Q7ym50	galbulimima	
1079	110	4.0	732	2	Q95D25	Q95d25	magnolia	ka
1080	110	4.0	732	2	Q95D46	Q95d46	pachylarnax	
1081	110	4.0	732	2	Q95D81	Q95d81	magnolia	li
1082	110	4.0	732	2	Q95D84	Q95d84	magnolia	cy
1083	110	4.0	732	2	Q95D92	Q95d92	magnolia	de
1084	110	4.0	732	2	Q95DA4	Q95da4	manglietia	
1085	110	4.0	732	2	Q95DA5	Q95da5	magnolia	ni
1086	110	4.0	732	2	Q95DA6	Q95da6	magnolia	ni
1087	109.5	4.0	372	2	Q83ZB1	Q83zb1	escherichia	
1088	109.5	4.0	403	2	Q8E0Q4	Q8e0q4	streptococc	
1089	109.5	4.0	428	2	Q935Z8	Q935z8	streptomyce	
1090	109.5	4.0	439	2	Q7NHW5	Q7nhw5	gloeobacter	
1091	109.5	4.0	443	2	Q9L4U6	Q9l4u6	streptomyce	
1092	109.5	4.0	504	2	Q95GT9	Q95gt9	nepenthes	m
1093	109.5	4.0	504	2	Q95GV4	Q95gv4	nepenthes	e
1094	109.5	4.0	598	2	Q97ES3	Q97es3	clostridium	
1095	109.5	4.0	678	2	Q9AM85	Q9am85	riemerella	
1096	109	3.9	324	2	Q69SI6	Q69si6	oryza	sativ
1097	109	3.9	408	2	P96564	P96564	amycolatops	
1098	109	3.9	426	2	Q8RS24	Q8rs24	streptomyce	

1099	109	3.9	669	2	Q95AS2	Q95as2	leopoldinia
1100	109	3.9	732	2	Q95D95	Q95d95	magnolia am
1101	109	3.9	732	2	Q95DA7	Q95da7	magnolia wi
1102	109	3.9	1684	2	Q7RJC0	Q7rjc0	plasmodium
1103	108.5	3.9	503	2	Q95GR3	Q95gr3	nepenthes m
1104	108.5	3.9	504	2	Q95GP3	Q95gp3	nepenthes f
1105	108.5	3.9	504	2	Q95GP9	Q95gp9	nepenthes e
1106	108.5	3.9	504	2	Q95GQ0	Q95gq0	nepenthes s
1107	108.5	3.9	504	2	Q95GQ6	Q95gq6	nepenthes s
1108	108.5	3.9	504	2	Q95GQ7	Q95gq7	nepenthes b
1109	108.5	3.9	504	2	Q95GQ9	Q95gq9	nepenthes p
1110	108.5	3.9	504	2	Q95GS0	Q95gs0	nepenthes b
1111	108.5	3.9	504	2	Q95GS3	Q95gs3	nepenthes a
1112	108.5	3.9	504	2	Q95GV0	Q95gv0	nepenthes l
1113	108.5	3.9	504	2	Q95GV1	Q95gv1	nepenthes i
1114	108.5	3.9	504	2	Q95GV7	Q95gv7	nepenthes g
1115	108.5	3.9	697	2	Q716U1	Q716u1	elegia fene
1116	108.5	3.9	705	2	Q9GHQ1	Q9ghq1	pseudonemac
1117	108.5	3.9	1232	1	Y908_METJA	Q58318	methanococc
1118	108	3.9	482	2	Q8LEW0	Q8lew0	arabidopsis
1119	108	3.9	488	2	Q84MN5	Q84mn5	oryza sativ
1120	108	3.9	499	2	Q6Z4K7	Q6z4k7	oryza sativ
1121	108	3.9	525	2	Q67GP6	Q67gp6	japonolirio
1122	108	3.9	688	2	Q6Y1U5	Q6ylu5	japonolirio
1123	108	3.9	708	2	Q9BAQ6	Q9baq6	styloceras
1124	108	3.9	732	2	Q95D32	Q95d32	magnolia po
1125	108	3.9	732	2	Q95D34	Q95d34	magnolia pa
1126	108	3.9	732	2	Q95D98	Q95d98	magnolia ta
1127	108	3.9	732	2	Q95D99	Q95d99	magnolia sh
1128	108	3.9	732	2	Q95DA0	Q95da0	magnolia gu
1129	108	3.9	732	2	Q95DA2	Q95da2	magnolia vi
1130	108	3.9	1097	2	O13592	O13592	saccharomyc
1131	108	3.9	1218	2	Q8VAV7	Q8vav7	white spot
1132	108	3.9	1219	2	Q8QTD0	Q8qtd0	white spot
1133	108	3.9	1219	2	Q91LB1	Q91lb1	white spot
1134	108	3.9	3079	1	IRA2_YEAST	P19158	saccharomyc
1135	107.5	3.9	403	2	Q9RPK3	Q9rpk3	streptococc
1136	107.5	3.9	504	2	Q95GP5	Q95gp5	nepenthes m
1137	107.5	3.9	504	2	Q95GQ4	Q95gq4	nepenthes t
1138	107.5	3.9	504	2	Q95GR0	Q95gr0	nepenthes f
1139	107.5	3.9	504	2	Q95GV3	Q95gv3	nepenthes s
1140	107.5	3.9	635	2	Q7YM60	Q7ym60	persea amer
1141	107.5	3.9	690	2	Q8M9S2	Q8m9s2	erica carne
1142	107.5	3.9	724	2	Q9TJZ6	Q9tjz6	alseis lugo
1143	107.5	3.9	732	2	Q9TJP3	Q9tjp3	simira viri
1144	107.5	3.9	732	2	Q9TJS2	Q9tjs2	pentagonia
1145	107	3.9	369	1	MURG_CLOTE	Q893r7	clostridium
1146	107	3.9	379	1	Y452_METAC	Q8tti1	methanosarc
1147	107	3.9	427	1	MURE_CAMJE	O69290	campylobact
1148	107	3.9	501	2	Q7YKK6	Q7ykk6	utricularia
1149	107	3.9	691	2	Q95AS8	Q95as8	wendlandiel
1150	107	3.9	694	2	Q95AQ6	Q95aq6	beccariopho
1151	107	3.9	695	2	Q95AR8	Q95ar8	reinhardtia
1152	107	3.9	698	2	Q95AR9	Q95ar9	podococcus
1153	107	3.9	698	2	Q95AS7	Q95as7	hyophorbe l
1154	107	3.9	698	2	Q95AU4	Q95au4	nypa frutic
1155	107	3.9	732	2	Q95D29	Q95d29	magnolia pa

1156	107	3.9	732	2	Q95D31	Q95d31	magnolia il
1157	107	3.9	732	2	Q95D47	Q95d47	manglietia
1158	107	3.9	732	2	Q95D48	Q95d48	manglietia
1159	107	3.9	732	2	Q95D49	Q95d49	manglietia
1160	107	3.9	732	2	Q95D50	Q95d50	manglietia
1161	107	3.9	732	2	Q95D51	Q95d51	manglietia
1162	107	3.9	732	2	Q95D52	Q95d52	manglietia
1163	107	3.9	732	2	Q95D53	Q95d53	manglietia
1164	107	3.9	732	2	Q95D54	Q95d54	manglietia
1165	107	3.9	732	2	Q95D55	Q95d55	manglietia
1166	107	3.9	732	2	Q95D56	Q95d56	manglietia
1167	107	3.9	732	2	Q95D57	Q95d57	manglietia
1168	107	3.9	732	2	Q95D58	Q95d58	manglietia
1169	106.5	3.8	376	2	Q8KND7	Q8knd7	micromonosp
1170	106.5	3.8	391	2	Q9RP99	Q9rp99	streptomyce
1171	106.5	3.8	419	2	Q6U850	Q6u850	mycobacteri
1172	106.5	3.8	421	2	O33935	O33935	saccharopol
1173	106.5	3.8	421	2	O54224	O54224	saccharopol
1174	106.5	3.8	428	2	Q83WE1	Q83we1	micromonosp
1175	106.5	3.8	504	2	Q95GQ3	Q95gq3	nepenthes v
1176	106.5	3.8	504	2	Q95GR9	Q95gr9	nepenthes t
1177	106.5	3.8	504	2	Q95GT8	Q95gt8	nepenthes p
1178	106.5	3.8	726	2	Q8M8V3	Q8m8v3	torricellia
1179	106.5	3.8	732	2	Q9TJT9	Q9tjt9	emmenoptery
1180	106.5	3.8	1243	2	Q74N29	Q74n29	nanoarchaeu
1181	106	3.8	388	2	O33282	O33282	mycobacteri
1182	106	3.8	388	2	Q7TY01	Q7ty01	mycobacteri
1183	106	3.8	414	2	Q7WQ52	Q7wq52	bordetella
1184	106	3.8	420	2	Q7D6N9	Q7d6n9	mycobacteri
1185	106	3.8	426	2	O87830	O87830	streptomyce
1186	106	3.8	440	2	Q8VWB7	Q8vwb7	streptomyce
1187	106	3.8	482	2	Q9ZUV0	Q9zuv0	arabidopsis
1188	106	3.8	501	2	Q7YKJ2	Q7ykJ2	utricularia
1189	106	3.8	677	2	Q7YM52	Q7ym52	degeneria r
1190	106	3.8	694	2	Q95AP8	Q95ap8	scheelea bu
1191	106	3.8	694	2	Q95AP9	Q95ap9	orbignya ba
1192	106	3.8	694	2	Q716V2	Q716v2	maianthemum
1193	106	3.8	695	2	Q95AQ5	Q95aq5	allagoptera
1194	106	3.8	695	2	Q95AS1	Q95as1	manicaria s
1195	106	3.8	696	2	Q95AQ0	Q95aq0	voanioala g
1196	106	3.8	696	2	Q95AQ4	Q95aq4	butia erios
1197	106	3.8	697	2	Q95AU3	Q95au3	thrinax rad
1198	106	3.8	698	2	Q95AQ1	Q95aq1	syagrus gla
1199	106	3.8	698	2	Q95AQ2	Q95aq2	lytocaryum
1200	106	3.8	698	2	Q95AQ3	Q95aq3	cocos nucif
1201	106	3.8	698	2	Q95AQ8	Q95aq8	barcella od
1202	106	3.8	698	2	Q95AR3	Q95ar3	aiphanes ac
1203	106	3.8	698	2	Q95AR6	Q95ar6	prestoea ac
1204	106	3.8	698	2	Q95AR7	Q95ar7	oenocarpus
1205	106	3.8	698	2	Q95AT5	Q95at5	dypsis last
1206	106	3.8	698	2	Q95AU0	Q95au0	phoenix dac
1207	106	3.8	732	2	Q95DC7	Q95dc7	magnolia al
1208	105.5	3.8	372	2	Q8L7Q5	Q8l7q5	arabidopsis
1209	105.5	3.8	372	2	Q712Q2	Q712q2	escherichia
1210	105.5	3.8	484	2	Q9ZQG4	Q9zqg4	arabidopsis
1211	105.5	3.8	504	2	Q95GU4	Q95gu4	nepenthes r
1212	105.5	3.8	504	2	Q95GU6	Q95gu6	nepenthes c

1213	105.5	3.8	556	2	Q03899	Q03899	saccharomyc
1214	105.5	3.8	570	2	Q9C9B0	Q9c9b0	arabidopsis
1215	105.5	3.8	624	2	Q95AY9	Q95ay9	osmorhiza b
1216	105.5	3.8	648	2	Q95AG6	Q95ag6	osmorhiza l
1217	105.5	3.8	667	2	Q7M9D4	Q7m9d4	wolinella s
1218	105.5	3.8	695	2	Q8WJZ9	Q8wjz9	baloskion t
1219	105.5	3.8	697	2	Q659X8	Q659x8	escherichia
1220	105.5	3.8	732	2	O98707	O98707	mussaenda e
1221	105.5	3.8	732	2	Q9TJS0	Q9tjs0	pogonopus s
1222	105.5	3.8	732	2	Q9TJV8	Q9tjv8	chimarrhis
1223	105.5	3.8	746	2	Q9TL72	Q9tl72	pittosporum
1224	105.5	3.8	749	2	Q9TL70	Q9tl70	hedera heli
1225	105.5	3.8	1275	2	Q9VAE1	Q9vae1	drosophila
1226	105	3.8	200	2	Q8GSQ9	Q8gsq9	triticum ae
1227	105	3.8	408	2	P96565	P96565	amycolatops
1228	105	3.8	429	2	Q9GFH3	Q9gfh3	liriodendro
1229	105	3.8	431	2	Q9MS90	Q9ms90	austrobaile
1230	105	3.8	625	2	Q8WI66	Q8wi66	cyrtostachy
1231	105	3.8	636	2	Q8WI64	Q8wi64	howea belmo
1232	105	3.8	666	2	Q6Y1V6	Q6ylv6	ophiopogon
1233	105	3.8	670	2	Q6Y1T4	Q6ylt4	serenoa sp.
1234	105	3.8	671	2	Q8WI77	Q8wi77	archontopho
1235	105	3.8	674	2	Q6Y1T5	Q6ylt5	dasypogon b
1236	105	3.8	678	2	Q8WI76	Q8wi76	clinostigma
1237	105	3.8	680	2	Q8WI67	Q8wi67	burretioken
1238	105	3.8	681	2	Q6Y1U9	Q6ylu9	aponogeton
1239	105	3.8	687	2	Q6Y1V5	Q6ylv5	polygonatum
1240	105	3.8	688	2	Q6Y1V3	Q6ylv3	cyanella hy
1241	105	3.8	688	2	Q6Y1V4	Q6ylv4	polygonatum
1242	105	3.8	689	2	Q67GP2	Q67gp2	dasypogon h
1243	105	3.8	696	2	Q95AR0	Q95ar0	desmoncus o
1244	105	3.8	696	2	Q95AT7	Q95at7	aphandra na
1245	105	3.8	697	2	Q95AS4	Q95as4	iriarte de
1246	105	3.8	697	2	Q95AU1	Q95au1	livistona s
1247	105	3.8	698	2	Q8WI62	Q8wi62	oncosperma
1248	105	3.8	698	2	Q8WI63	Q8wi63	hydriastele
1249	105	3.8	698	2	Q8WI65	Q8wi65	gronophyllu
1250	105	3.8	698	2	Q8WI68	Q8wi68	bentinckia
1251	105	3.8	698	2	Q8WI75	Q8wi75	linospadix
1252	105	3.8	698	2	Q95AR4	Q95ar4	acrocomia a
1253	105	3.8	698	2	Q95AS5	Q95as5	ravenea hil
1254	105	3.8	698	2	Q95AT3	Q95at3	chambeyroni
1255	105	3.8	698	2	Q95AU2	Q95au2	washingtoni
1256	105	3.8	699	2	Q6A2L5	Q6a2l5	campylanthu
1257	105	3.8	700	2	Q95AT6	Q95at6	phytelephas
1258	105	3.8	732	2	Q95D82	Q95d82	magnolia ac
1259	105	3.8	732	2	Q95D83	Q95d83	magnolia ac
1260	104.5	3.8	419	2	Q6U852	Q6u852	mycobacteri
1261	104.5	3.8	419	2	Q6U862	Q6u862	mycobacteri
1262	104.5	3.8	427	2	Q98EL9	Q98el9	rhizobium l
1263	104.5	3.8	428	2	Q8GEA2	Q8gea2	mycobacteri
1264	104.5	3.8	435	2	Q8LGD9	Q8lgd9	arabidopsis
1265	104.5	3.8	454	2	Q6VAA3	Q6vaa3	stevia reba
1266	104.5	3.8	504	2	Q95GS4	Q95gs4	nepenthes t
1267	104.5	3.8	504	2	Q95GU0	Q95gu0	nepenthes m
1268	104.5	3.8	504	2	Q95GU8	Q95gu8	nepenthes l
1269	104.5	3.8	640	2	Q71N60	Q71n60	stimpsonia

1270	104.5	3.8	671	2	Q85XZ9	Q85xz9	trevesia lo
1271	104.5	3.8	681	2	Q85Y02	Q85y02	trevesia pa
1272	104.5	3.8	682	2	Q85Y07	Q85y07	trevesia ba
1273	104.5	3.8	707	2	Q85Y00	Q85y00	trevesia pa
1274	104.5	3.8	707	2	Q85Y01	Q85y01	trevesia pa
1275	104.5	3.8	707	2	Q85Y03	Q85y03	trevesia su
1276	104.5	3.8	732	2	Q9TJP1	Q9tjpl	warszewiczi
1277	104.5	3.8	736	2	Q7YU76	Q7yu76	drosophila
1278	104.5	3.8	749	2	Q9TL66	Q9tl66	helwingia j
1279	104	3.8	417	2	Q9F832	Q9f832	micromonosp
1280	104	3.8	695	2	Q95AR1	Q95ar1	batricis hum
1281	104	3.8	698	2	Q95AR2	Q95ar2	astrocaryum
1282	104	3.8	698	2	Q6Q962	Q6q962	uncultured
1283	104	3.8	732	2	Q95D44	Q95d44	liriodendro
1284	104	3.8	732	2	Q9TL43	Q9tl43	liriodendro
1285	104	3.8	795	2	Q6BWH4	Q6bwh4	debaryomyce
1286	104	3.8	856	2	Q6X9R1	Q6x9r1	dictyoglomu
1287	104	3.8	1026	2	Q86T84	Q86t84	homo sapien
1288	103.5	3.7	371	2	Q79ST1	Q79st1	salmonella
1289	103.5	3.7	371	2	P96056	P96056	salmonella
1290	103.5	3.7	371	2	Q8ZMN4	Q8zmn4	salmonella
1291	103.5	3.7	422	2	Q9RMP3	Q9rmp3	mycobacteri
1292	103.5	3.7	448	2	Q9LPS8	Q9lps8	arabidopsis
1293	103.5	3.7	465	2	Q8LP23	Q8lp23	nierembergi
1294	103.5	3.7	469	1	NTRC_KLEPN	P03029	klebsiella
1295	103.5	3.7	503	2	Q95GP8	Q95gp8	nepenthes m
1296	103.5	3.7	504	2	Q95GU5	Q95gu5	nepenthes c
1297	103.5	3.7	642	2	Q8SLR5	Q8slr5	clethra bar
1298	103.5	3.7	684	2	Q85XZ5	Q85xz5	oplopanax h
1299	103.5	3.7	695	2	Q9TJS9	Q9tjs9	mussaenda a
1300	103.5	3.7	701	2	Q85XZ8	Q85xz8	trevesia bu
1301	103.5	3.7	714	2	Q9SC96	Q9sc96	melanophyll
1302	103.5	3.7	739	2	Q8FA89	Q8fa89	escherichia
1303	103.5	3.7	1489	2	Q6CNY4	Q6cny4	kluveromyce
1304	103	3.7	395	2	Q66B02	Q66b02	yersinia ps
1305	103	3.7	395	2	Q8ZF10	Q8zf10	yersinia pe
1306	103	3.7	440	2	Q9L555	Q9l555	streptomyce
1307	103	3.7	508	1	TNSD_ECOLI	P13991	escherichia
1308	103	3.7	563	2	Q9FWC1	Q9fwc1	oryza sativ
1309	103	3.7	626	2	Q9XYR4	Q9xyr4	schistosoma
1310	103	3.7	670	2	Q8HUP0	Q8hup0	convallaria
1311	103	3.7	695	2	Q95AT1	Q95at1	calyptronom
1312	103	3.7	697	2	Q95AU6	Q95au6	calamus cae
1313	103	3.7	698	2	Q95AQ9	Q95aq9	gastrococos
1314	103	3.7	698	2	Q95AS3	Q95as3	wettinia hi
1315	103	3.7	732	2	Q95CW5	Q95cw5	magnolia el
1316	103	3.7	966	1	AMPN_HUMAN	P15144	homo sapien
1317	102.5	3.7	389	2	Q6QR18	Q6qr18	streptomyce
1318	102.5	3.7	435	2	Q9LNE6	Q9lne6	arabidopsis
1319	102.5	3.7	500	2	Q6BKR3	Q6bkr3	debaryomyce
1320	102.5	3.7	501	2	Q95GP4	Q95gp4	nepenthes l
1321	102.5	3.7	504	2	Q95GT7	Q95gt7	nepenthes d
1322	102.5	3.7	622	1	PPCC_HUMAN	P35558	homo sapien
1323	102.5	3.7	653	2	Q95AY4	Q95ay4	anthriscus
1324	102.5	3.7	663	2	Q97YG8	Q97yg8	sulfolobus
1325	102.5	3.7	684	2	Q8WK00	Q8wk00	elegia stip
1326	102.5	3.7	688	2	Q716W1	Q716w1	trichopus s

1327	102.5	3.7	700	2	Q85VG8	Q85vg8	brassaiopsi
1328	102.5	3.7	706	2	Q98S94	Q98s94	guillardia
1329	102.5	3.7	735	2	Q9TL73	Q9tl73	osmorhiza c
1330	102.5	3.7	749	2	Q9TL74	Q9tl74	coriandrum
1331	102.5	3.7	816	2	Q7XMH8	Q7xmh8	oryza sativ
1332	102.5	3.7	1275	1	TRP_DROME	P19334	drosophila
1333	102.5	3.7	1456	2	Q8NJS1	Q8njs1	leptosphaer
1334	102.5	3.7	3001	2	Q8QXL0	Q8qxl0	scallion mo
1335	102	3.7	300	2	Q7MFU3	Q7mfu3	vibrio vuln
1336	102	3.7	334	2	Q9RTN6	Q9rtn6	deinococcus
1337	102	3.7	390	2	Q9RN61	Q9rn61	streptomyce
1338	102	3.7	443	2	Q9GFH4	Q9gfh4	lactoris fe
1339	102	3.7	609	2	Q7XRN9	Q7xrn9	oryza sativ
1340	102	3.7	647	2	Q7YM57	Q7ym57	anaxagorea
1341	102	3.7	670	2	Q6JX97	Q6jx97	sparattosyc
1342	102	3.7	676	2	Q9TL41	Q9tl41	ceratophyll
1343	102	3.7	694	2	O47210	O47210	cyanastrum
1344	102	3.7	718	2	Q7MBD5	Q7mbd5	chromobacte
1345	102	3.7	732	2	Q9TL42	Q9tl42	magnolia si
1346	102	3.7	1655	1	N188_YEAST	P52593	saccharomyc
1347	101.5	3.7	291	2	Q6MUK0	Q6muk0	mycoplasma
1348	101.5	3.7	351	2	Q9FKD1	Q9fkd1	arabidopsis
1349	101.5	3.7	371	2	Q6KD92	Q6kd92	escherichia
1350	101.5	3.7	385	1	MURG_RICPR	Q9zdc0	rickettsia
1351	101.5	3.7	387	2	Q8FIW3	Q8fiw3	escherichia
1352	101.5	3.7	436	2	Q9F839	Q9f839	micromonosp
1353	101.5	3.7	454	2	Q8H6A4	Q8h6a4	stevia reba
1354	101.5	3.7	512	2	Q95GU7	Q95gu7	nepenthes l
1355	101.5	3.7	646	2	Q8SLR6	Q8slr6	clethra arb
1356	101.5	3.7	684	2	Q85Y11	Q85y11	brassaiopsi
1357	101.5	3.7	694	2	Q85Y04	Q85y04	hedera heli
1358	101.5	3.7	695	2	Q85XZ6	Q85xz6	macropanax
1359	101.5	3.7	696	2	Q9TL87	Q9tl87	cyananthus
1360	101.5	3.7	698	2	Q85Y12	Q85y12	brassaiopsi
1361	101.5	3.7	700	2	Q85UX5	Q85ux5	brassaiopsi
1362	101.5	3.7	701	2	Q85Y10	Q85y10	brassaiopsi
1363	101.5	3.7	703	2	Q85XZ4	Q85xz4	eleutheroco
1364	101.5	3.7	704	2	Q85Y08	Q85y08	brassaiopsi
1365	101.5	3.7	705	2	Q85Y06	Q85y06	fatsia japo
1366	101.5	3.7	705	2	Q85Y13	Q85y13	brassaiopsi
1367	101.5	3.7	707	2	Q85Y05	Q85y05	brassaiopsi
1368	101.5	3.7	714	2	Q8MC77	Q8mc77	aralidium p
1369	101.5	3.7	725	2	Q8MC69	Q8mc69	aralia spin
1370	101.5	3.7	728	2	O98702	O98702	luculia gra
1371	101.5	3.7	732	2	Q9TJS5	Q9tjs5	pseudomussa
1372	101.5	3.7	732	2	Q9TJY6	Q9tjy6	capirona de
1373	101.5	3.7	732	2	Q9TJZ4	Q9tjz4	alberta mag
1374	101.5	3.7	734	2	Q9THY8	Q9thy8	gardenia th
1375	101.5	3.7	741	2	Q9TL71	Q9tl71	eleutheroco
1376	101.5	3.7	748	2	Q9TL75	Q9tl75	angelica gi
1377	101.5	3.7	856	2	Q6MAY5	Q6may5	parachlamyd
1378	101	3.6	290	2	Q8D4B7	Q8d4b7	vibrio vuln
1379	101	3.6	339	2	Q6H8F8	Q6h8f8	oryza sativ
1380	101	3.6	340	2	Q7XW21	Q7xw21	oryza sativ
1381	101	3.6	386	2	Q73W10	Q73w10	mycobacteri
1382	101	3.6	393	2	O87480	O87480	streptomyce
1383	101	3.6	420	2	Q8MEI2	Q8mei2	malva negle

1384	101	3.6	511	1	VAT_TORMA	Q91498	torpedo mar
1385	101	3.6	641	2	Q7YM34	Q7ym34	zygogynum p
1386	101	3.6	687	2	Q6Y1X5	Q6ylx5	alania endl
1387	101	3.6	693	2	Q32231	Q32231	flagellaria
1388	101	3.6	695	2	Q6Y1U3	Q6ylu3	aletris far
1389	101	3.6	697	2	O03659	O03659	tetraclea c
1390	101	3.6	697	2	Q95AT0	Q95at0	geonoma oxy
1391	101	3.6	698	2	Q95AQ7	Q95aq7	elaeis olei
1392	101	3.6	699	2	Q716V5	Q716v5	croomia jap
1393	101	3.6	742	2	Q9TLC0	Q9tlc0	tetraclea c
1394	101	3.6	745	2	Q9TLC1	Q9tlc1	clerodendru
1395	101	3.6	1023	2	Q9XYD4	Q9xyd4	dictyosteli
1396	100.5	3.6	370	2	Q97MF5	Q97mf5	clostridium
1397	100.5	3.6	455	2	Q9ALN7	Q9aln7	saccharopol
1398	100.5	3.6	504	2	Q95GS7	Q95gs7	nepenthes n
1399	100.5	3.6	647	2	Q9GEU0	Q9geu0	samolus val
1400	100.5	3.6	717	2	Q8MC98	Q8mc98	apium grave
1401	100.5	3.6	720	2	Q8M9R5	Q8m9r5	eremosyne p
1402	100.5	3.6	732	2	Q32055	Q32055	campanula r
1403	100.5	3.6	741	2	Q9TL69	Q9tl69	panax ginse
1404	100.5	3.6	861	1	GCR3_YEAST	P34160	saccharomyc
1405	100.5	3.6	1066	2	Q6CU73	Q6cu73	kluveromyc
1406	100	3.6	230	2	Q81PS7	Q81ps7	bacillus an
1407	100	3.6	231	2	Q6HXZ4	Q6hxz4	bacillus an
1408	100	3.6	338	2	Q9MSP6	Q9msp6	nymphaea od
1409	100	3.6	415	2	Q7VGY0	Q7vgy0	helicobacte
1410	100	3.6	507	2	Q85XY9	Q85xy9	peganum har
1411	100	3.6	669	2	Q6JX92	Q6jx92	helicostyli
1412	100	3.6	680	2	Q6Y1U7	Q6ylu7	halodule wr
1413	100	3.6	687	2	Q6Y1U8	Q6ylu8	gymnostachy
1414	100	3.6	690	2	Q6Y1V1	Q6ylv1	xeronema ca
1415	100	3.6	690	2	Q9BAS2	Q9bas2	buxus hilde
1416	100	3.6	693	2	Q85XZ7	Q85xz7	dendropanax
1417	100	3.6	694	2	Q67GN4	Q67gn4	blandfordia
1418	100	3.6	709	2	Q9BAR8	Q9bar8	sarcococca
1419	100	3.6	1026	2	Q86T76	Q86t76	homo sapien
1420	100	3.6	1058	2	Q9PCW4	Q9pcw4	xylella fas
1421	100	3.6	2543	2	Q63CQ7	Q63cq7	bacillus ce
1422	100	3.6	3392	2	Q7ZA38	Q7za38	ashbya goss
1423	99.5	3.6	348	2	Q87SS3	Q87ss3	vibrio para
1424	99.5	3.6	370	2	Q93GK9	Q93gk9	klebsiella
1425	99.5	3.6	371	2	Q8GH22	Q8gh22	escherichia
1426	99.5	3.6	392	2	Q86D27	Q86d27	entamoeba h
1427	99.5	3.6	396	2	O29653	O29653	archaeoglob
1428	99.5	3.6	518	2	Q8D366	Q8d366	wiggleswort
1429	99.5	3.6	622	1	PPCC_MOUSE	Q9z2v4	mus musculu
1430	99.5	3.6	622	2	Q8BSX3	Q8bsx3	mus musculu
1431	99.5	3.6	622	2	Q8CI37	Q8ci37	mus musculu
1432	99.5	3.6	670	2	Q8HUN8	Q8hun8	ipheion dia
1433	99.5	3.6	679	2	Q8WGU3	Q8wgu3	pennantia c
1434	99.5	3.6	701	2	Q9SC21	Q9sc21	sollya hete
1435	99.5	3.6	716	2	Q85UX6	Q85ux6	brassaiopsi
1436	99.5	3.6	735	2	Q8WGU6	Q8wgu6	pennantia c
1437	99.5	3.6	1144	2	Q6MF68	Q6mf68	parachlamyd
1438	99	3.6	74	2	Q941P3	Q94lp3	arachis hyp
1439	99	3.6	190	2	O62371	O62371	caenorhabdi
1440	99	3.6	343	2	Q73CT7	Q73ct7	bacillus ce

1441	99	3.6	371	2	Q6U5X7	Q6u5x7	klebsiella
1442	99	3.6	429	2	Q9GFH2	Q9gfh2	saururus ce
1443	99	3.6	439	2	Q62CH1	Q62ch1	burkholderi
1444	99	3.6	493	2	Q8CWG5	Q8cwg5	yersinia pe
1445	99	3.6	504	2	Q95GS2	Q95gs2	nepenthes n
1446	99	3.6	612	2	Q6UQ74	Q6uq74	sinningia s
1447	99	3.6	627	2	Q7YM46	Q7ym46	cephalospha
1448	99	3.6	659	2	Q7YM36	Q7ym36	virola sebi
1449	99	3.6	665	2	Q9GGT9	Q9ggt9	dulichium a
1450	99	3.6	676	2	Q7YM40	Q7ym40	knema lauri
1451	99	3.6	676	2	Q7YM43	Q7ym43	gymnacranth
1452	99	3.6	680	2	Q8WI61	Q8wi61	ptychosperm
1453	99	3.6	680	2	Q7YM38	Q7ym38	myristica f
1454	99	3.6	684	2	Q8HUP1	Q8hup1	asparagus f
1455	99	3.6	686	2	P92299	P92299	glechoma he
1456	99	3.6	686	2	P92329	P92329	plectranthu
1457	99	3.6	707	2	Q9GHZ4	Q9ghz4	chaenorhinu
1458	99	3.6	707	2	Q9MVJ0	Q9mvj0	heritiera l
1459	99	3.6	708	2	Q9GHW4	Q9ghw4	gambelia sp
1460	99	3.6	738	2	O19931	O19931	tetrachondr
1461	99	3.6	1058	2	Q9VP94	Q9vp94	drosophila
1462	99	3.6	2485	2	Q7RRE3	Q7rre3	plasmodium
1463	99	3.6	3392	2	Q75AD9	Q75ad9	ashbya goss
1464	98.5	3.6	371	2	Q67DV4	Q67dv4	shigella dy
1465	98.5	3.6	371	2	Q83WA1	Q83wa1	escherichia
1466	98.5	3.6	383	2	Q7WC49	Q7wc49	bordetella
1467	98.5	3.6	606	2	Q6FRS6	Q6frs6	candida gla
1468	98.5	3.6	700	2	Q9TLF5	Q9tlf5	globularia
1469	98.5	3.6	732	2	Q9TJY9	Q9tjy9	calycophyll
1470	98.5	3.6	733	2	O19941	O19941	globularia
1471	98.5	3.6	942	2	P74081	P74081	synechocyst
1472	98.5	3.6	1049	1	VP39_YEAST	Q07468	saccharomyc
1473	98.5	3.6	1656	2	Q7R489	Q7r489	giardia lam
1474	98.5	3.6	3645	2	Q750B4	Q750b4	ashbya goss
1475	98	3.5	230	2	Q6KS13	Q6ks13	bacillus an
1476	98	3.5	307	2	Q7XXJ7	Q7xxj7	oryza sativ
1477	98	3.5	343	2	Q81UI1	Q81ui1	bacillus an
1478	98	3.5	346	2	Q6I2Q8	Q6i2q8	bacillus an
1479	98	3.5	373	2	Q8KUL2	Q8kul2	streptococc
1480	98	3.5	379	2	Q8NLS7	Q8nls7	corynebacte
1481	98	3.5	382	2	Q9ZA43	Q9za43	streptomyce
1482	98	3.5	391	1	CAPJ_STAAU	P39859	staphylococ
1483	98	3.5	408	2	Q73TF6	Q73tf6	mycobacteri
1484	98	3.5	442	2	Q53881	Q53881	streptomyce
1485	98	3.5	444	2	Q8F9G4	Q8f9g4	leptospira
1486	98	3.5	543	2	Q7YXZ2	Q7yxz2	cryptospori
1487	98	3.5	622	1	PPCC_CHICK	P05153	gallus gall
1488	98	3.5	623	2	Q7YM41	Q7ym41	iryanthera
1489	98	3.5	636	2	Q716U7	Q716u7	stichoneuro
1490	98	3.5	667	2	Q6JX80	Q6jx80	perebea gui
1491	98	3.5	669	2	Q8HUN9	Q8hun9	agapanthus
1492	98	3.5	670	2	Q6JXA8	Q6jxa8	batocarpus
1493	98	3.5	671	2	Q8HUN6	Q8hun6	narcissus e
1494	98	3.5	672	2	Q95AT4	Q95at4	areca vesti
1495	98	3.5	686	2	Q6Y1V2	Q6ylv2	tecophilaea
1496	98	3.5	688	2	Q6Y1V9	Q6ylv9	dracaena au
1497	98	3.5	690	2	Q6Y1W6	Q6ylw6	hypoxis jun

1498	98	3.5	692	2	Q67GN8	Q67gn8 roystonea p
1499	98	3.5	694	2	O47200	O47200 narcissus e
1500	98	3.5	697	2	Q95AR5	Q95ar5 roystonea o

ALIGNMENTS

RESULT 1

Q6UXC4

ID Q6UXC4 PRELIMINARY; PRT; 523 AA.
AC Q6UXC4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glucuronosyltransferase.
GN ORFNames=UNQ842;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; AY358416; AAQ88782.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 523 AA; 59580 MW; 5DE9CD92D1FBA18F CRC64;

Query Match 100.0%; Score 2768; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 6.7e-210;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Dd	1	MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR	60
Qy	61	GPFPMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ	120

Db 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180
 |||

Db 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPIP 180

Qy 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
 |||

Db 181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300
 |||

Db 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL 300

Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360
 |||

Db 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 |||

Db 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
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Db 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
 |||

Db 481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523

RESULT 2

Q8NBP2

ID Q8NBP2 PRELIMINARY; PRT; 523 AA.

AC Q8NBP2;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein PSEC0073.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S., ...

RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,

RA Nagahari K., Sugano S., Isogai T.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.

DR EMBL; AK075383; BAC11583.1; -.

DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002213; UDP_glucos_trans.

DR Pfam; PF00201; UDPGT; 1.

DR PROSITE; PS00375; UDPGT; 1.

KW Glycosyltransferase; Transferase.

SQ SEQUENCE 523 AA; 59618 MW; 89928A26AB9C09F5 CRC64;

Query Match 99.5%; Score 2754; DB 2; Length 523;
Best Local Similarity 99.6%; Pred. No. 8.5e-209;
Matches 521; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60

Qy     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFSGSLEFGLPIP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVFVAILSTSFSGSLEFGLPIP 180

Qy    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHL 240

Qy    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVQDLENFIAKFGDSGFVLVTL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVQDLENFIAKFEDSGFVLVTL 300

Qy    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAH 360

Qy    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETL 420

Qy    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480

Qy    481 HEQYLFDFVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
        ||||| ||||||||||||||||||||||||||||||||||||||||
Db    481 HEQYLLDVFLGLTLGLTLWLCGKLLGMAVWWLRGARKVKET 523
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RESULT 3

Q6NUS8

ID Q6NUS8 PRELIMINARY; PRT; 523 AA.

AC Q6NUS8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein FLJ34658.

GN Name=FLJ34658;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

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RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      Strausberg R.;
RL      Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR      EMBL; BC068446; AAH68446.1; -.
DR      GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR002213; UDP_glucos_trans.
DR      Pfam; PF00201; UDPGT; 1.
DR      PROSITE; PS00375; UDPGT; 1.
KW      Glycosyltransferase; Hypothetical protein; Transferase.
SO      SEQUENCE      523 AA;  59150 MW;  602AE3D75CE986BD CRC64;

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RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; AK057066; BAB71358.1; -.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Transferase.
SO SEQUENCE 523 AA; 59148 MW; 2034D6E90863EA8E CRC64;

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Qy	1	MAGQRVLLLVGFLLPVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR	60
Db	1	MVGQRVLLLVAFLLSGVLLSEAAKILTISTLGGSHYLLLD RVSQILQE HGHNV TML-HQS	59
Qy	61	GPFM-PDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLAL	119
Db	60	GKFLIPDIKEEEKSYQVIRWFSPEDHQKRIKKHFDSYIETALDGRKESEALVKLMEIFGT	119
Qy	120	QCSHF LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKL GKPFVAILSTSF G SLEFGLPI	179
Db	120	QCSYLLSRKDIMDSLKNENCDLVFVEAFDFCSFLIAEKL VKPFVAILPTTFGSLDFGLPS	179
Qy	180	PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSH	239
Db	180	PLSYVPVFPSLLTDHMDFWGRVKNFLMFFSFSRSQWDMQSTFDNTIKEHFPEGSRPVLSH	239
Qy	240	LLLKAELWFINSDFAFDFARPLL PNTVYVGGLMEKPIKPV PQDLENFIAKFGDSGFVLVT	299
Db	240	LLLKAELWFVNSDFAFDFARPLL PNTVYIGGLMEKPIKPV PQDLNFIANFGDAGFVLVA	299
Qy	300	LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA	359
Db	300	FGSMLNTHQSQEVLKKMHNAFAHLPQGVWITCQSSHWPRDVHLATNVKIVDWLPQSDLLA	359
Qy	360	HPSIRLFVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAET	419
Db	360	HPSIRLFVTHGGQNSVME TIRHGVPMVGLPVNGDQHGMNVRVVAKNYGVSI RL NQVTADT	419
Qy	420	LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQP	479
Db	420	LTILTMKOVIEDKRYKSAVVAASVILHSQPLSPAORLVGWIDHILQTGGATHLKPYVFQQP	479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWVLRGARKVKET 523
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 Db 480 WHEQYLIDVFLGLTLGLTMWLCLGKLLGVVARWLRGARKVKKT 523

RESULT 5

Q8ROY5

ID Q8ROY5 PRELIMINARY; PRT; 523 AA.
 AC Q8ROY5;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Expressed sequence AI746432.
 GN Name=AI746432;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 DR EMBL; BC025940; AAH25940.1; -.
 DR MGD; MGI:2146055; AI746432.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_glucos_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Glycosyltransferase; Transferase.

SQ SEQUENCE 523 AA; 59742 MW; F2EF34F41C3DEB95 CRC64;

Query Match 65.6%; Score 1815; DB 2; Length 523;

Best Local Similarity 65.4%; Pred. No. 1.3e-134;

Matches 342; Conservative 73; Mismatches 106; Indels 2; Gaps 2;

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Qy      1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHR 60
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Db      1 MAAHRSWLLVSFFLLEVLLEAAKILTISTLSASHYILMNRVSQILQGGGHDVIKLLYEG 60

Qy     61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
      | :||:| | ||||:| ||| |: |: : :|| || |: || : :| |
Db     61 GD-IPDFRKENS SYQVINWRLPEDQQKTFENRWHRLIDEYAYGRSKYHTLLKIHQYFADL 119

Qy    121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFSGSLEFGLP-I 179
      ||| |:| ||||: |: ||||:|:|:| | | ||| |||| ||: | | :|||
Db    120 CSHLLSRKDIMELLQKENFDLVLLDSMDLCSFLIVEKLKGRFVSFLPFQFSYMDFGLPNA 179

Qy    180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQHMQSTFDNTIKEHFTEGSRPVLSH 239
      |||| ||: | ||| ||||| |||| | :|:| : | : ||:| |||:| |||
Db    180 PLSYAPVYGSLTDQMDFWGRVKNILMFFHFTKKRRDIFSQYGNTVQEHFAEGSQPVLS 239

Qy    240 LLLKAELWFINSDFAFDFARPLLNTVYVGGLMKPKIPVPQDLENFIAKFGDSGFVLVT 299
      |||||:| |||| | |||| | |||||:|:|:|:|:| ||||:|:|:| |||||
Db    240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLEDFISQFGDSGFVLVA 299

Qy    300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQC SHWPKDVHLAANVKIVDWLPQSDLLA 359
      | |:|: |: || ||||:| |||||:| |: ||||| || ||||:| |||
Db    300 LDSVSMIQSKEIIKEMNSAFAHLPQGVLTCKSSHWPKDVSLAPNVKIMDWLPQIDLLA 359

Qy    360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
      ||||| |||| | |:| |: | ||||| | ||||| ||||| |||||: ||||:
Db    360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFGDQPENMVRVEAKNLGVSIQLQTLKAES 419

Qy    420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQP 479
      | ||:|:| |:| |:| |: | ||| |:| |||||:| ||||| |||| | |||
Db    420 FLLTMKEVIEDQRYKTAAMASKVIRNSHPLTPAQLVGWIDHILQTGGAAHLKPYAFQQP 479

Qy    480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
      ||||: ||:| ||||| |||| |:| :| :||:
Db    480 WHEQYMLDVFLFLLGLTLGLTLWLSVKVLVAVTRYLSISRKVQ 522
```

RESULT 6

Q8JZZ0

ID Q8JZZ0 PRELIMINARY; PRT; 523 AA.

AC Q8JZZ0;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein AI313915.

GN Name=AI313915;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; BC034837; AAH34837.1; -.
DR MGD; MGI:2145969; AI313915.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Hypothetical protein; Transferase.
SQ SEQUENCE 523 AA; 59662 MW; 4F7BD5ACBAFB5127 CRC64;

Query Match 65.2%; Score 1804; DB 2; Length 523;
Best Local Similarity 65.4%; Pred. No. 9.4e-134;
Matches 342; Conservative 69; Mismatches 110; Indels 2; Gaps 2;

Qy 1-MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
|| | ||: || | :| ||||| |||: |||: |||: | : |||| | : :
Db 1 MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

Qy 61 GPFMPDFKKEEKSYQVISWLPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
: |||: ||: |||||: | ||| : : | || || | || : : |
Db 61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGLP-I 179
|| | : ||||| |||||: |||: | | || |||| ||: | | : |||||
Db 120 CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGFLPSA 179

Qy 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSH 239
|||| ||: | ||| ||||| ||||| | : ||: | : |||: ||| |||: ||||

Db 180 PLSYAPVYGSGLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQPVLSD 239

Qy 240 LLLKAELWFINSDFAFDFARPLLNTVYVGGIMEKPIKPVPQDLENFIAKFGDSGFVLVT 299
 |||||:||||| ||||| |||||:|||||:|||||:|||||

Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLENFISQFGDSGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQC SHWPKDVHLAANVKIVDWLPQSDLLA 359
 |||:|: |: || ||||:|||||:| |: ||||| ||:||||:||||:||||

Db 300 LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTKTS HWPKDVSLASNKIMDWLPQTDLLA 359

Qy 360 HPSIRL FVTHGGQNSIMEAIQHGVPMVGIP LFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
 ||||| ||||| ||:||||: ||||| ||||| ||||| ||||| |||||: |||||

Db 360 HPSIRL FVTHGGMNSVMEAVHHGVPMVGIP PFFFDQPENMVRVEAKNLGVS IQLQTLKAES 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQP 479
 || ||:|:|||||:|: |: ||||:| |||:||||:||||| ||||| ||||

Db 420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRL LGWIDHILQTGGAAHLKPYAFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWL CGKLLGMAVWWLRGARKVKE 522
 |||||: |||:||||| ||||| |:| |:| | ||||

Db 480 WHEQYMLDVFLGLGLMLGTLWLSVKVLVAVTRYLSIATKVKE 522

RESULT 7

Q8VC11

ID Q8VC11 PRELIMINARY; PRT; 523 AA.

AC Q8VC11;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein AI313915 (Mus musculus adult male liver tumor

DE cDNA, RIKEN full-length enriched library, clone:C730018P11

DE product:hypothetical UDP-glucoronosyl and UDP-glucosyl transferase

DE containing protein, full insert sequence).

GN Name=AI313915;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [8]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR EMBL; BC022134; AAH22134.1; -.
DR EMBL; AK050128; BAC34080.1; -.
DR MGD; MGI:2145969; AI313915.
DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycosyltransferase; Hypothetical protein; Transferase.
SQ SEQUENCE 523 AA; 59672 MW; BC7BD6ADF197ADD9 CRC64;

Query Match 65.1%; Score 1802; DB 2; Length 523;
Best Local Similarity 65.4%; Pred. No. 1.4e-133;
Matches 342; Conservative 68; Mismatches 111; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
|| | ||: || |:| |||||: ||:: |||: | : |||| | :
Db 1 MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
: |||: ||: ||||: | ||| ::| || || | || : :|
Db 61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPVAILSTSFSGSLEFGLP-I 179
|| |:| |||| | |||||:|::: | | || |||| ||: | | :|||
Db 120 CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGFLPSA 179

Qy 180 PLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTGSRPVLSH 239
|||| ||: | || ||||| ||||| | :|: | :|:|:| |||: |||
Db 180 PLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQLPVLSD 239

Qy 240 LLLKAELWFINSDFAFDFAFPLLPNTVYVGGLMKPIKVPQDLENFIAKFGDSGFVLVT 299
|||||||: |||| | |||| | |||||:|:::|:|:|:| |||||:| |||||
Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVGGLLDKPVQPIPDLENFISQFGDSGFVLVA 299

Qy 300 LGSMVNTCQNPEIFKEMNNAFAHLPQGVWKQCQSHWPKDVHLAANVKIVDWLPQSDLLA 359
|||:|: |: || ||||: |||||:| |: ||||| || ||||: ||||: |||
Db 300 LGSIVSMIQSKEIIKEMNSAFAHLPQGVLTCTKSHWPKDVSLAPNVKIMDWLPQTDLLA 359

Qy 360 HPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFGDQPENMVRVEAKKFGVSIQLKKLKAET 419
||||||| ||: |||: ||||| | ||||| |||||: ||||: ||||
Db 360 HPSIRLFVTHGGMNSVMEAVHHGVPMVGIPFFFDQPENMVRVEAKNLGVSQQLTLKAES 419

Qy 420 LALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVFQQP 479
 || ||:|:|||||||:|: || |||:| |||:|||||:||||| |||| ||||
 Db 420 FALTMKKIIEDKRYKSAAMASKIIRHSHPLTPAQRLLGWIDHILQTGGAAHLKPYAFQQP 479

Qy 480 WHEQYLFDFVFLGLTLGLTLWLCLGKLLGMAVWWLRGARKVKE 522
 |||||: |||:|||| | |||| | :| :| | ||||
 Db 480 WHEQYMLDVFLFLGLMLGLTLWLSVKVLVAVTRYLSIATKVKE 522

RESULT 8

Q63ZR6

ID Q63ZR6 PRELIMINARY; PRT; 523 AA.
 AC Q63ZR6;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC082844; AAH82844.1; -.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 60436 MW; 73B728B7D1CE5CA0 CRC64;

Query Match 41.4%; Score 1145; DB 2; Length 523;
Best Local Similarity 42.4%; Pred. No. 1.1e-81;
Matches 224; Conservative 111; Mismatches 181; Indels 12; Gaps 4;

Qy 1 MAGQRVLLLVGFLLPGLVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKR 60
|| | |:: | : | | | | : | | | | | : | | : | | |
Db 1 MAVGRKSLILSLLIQHVFLLHGAKILTVCFLLGGSHYLLWMDEISRILHNNGQEVMTMFLQIA 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGR--GKFENLLNVLEYLA 118
: | | : : | | : | : | : : | : | : : : : : : : : : :
Db 61 DGLLPDYQMQUESPYRLITWSLTKNYLKEFS---EFFRDSKYNFKDCDELSSYLGLMTHFS 117

Qy 119 LQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPFVAI----LSTSFSGSLE 174
| | | : | | : | | : | : : : : | | : | | | | | : : : |
Db 118 RQCKMIFNQTSIMNLLKEEKYDLAVIDSFNPCTFLVSEKLGIPFIATHPPFPVKSPWHS-- 175

Qy 175 FGLPIPLSYVPVFRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSR 234
| : | | | : | : : | | | | | : | : : : : | : | : | : | |
Db 176 -GIPNQLSYMPVYQSQSLTDHMDFFERVKNVFMYIASAVLERKIYSLFDDVIEEHFPACSR 234

Qy 235 PVLSHLLKAEWLFINSDFAFDFARPLLPNTVYVGGLEMEKPIKVPQDLENFIAKFGDSG 294
| | | | | : | : | : | | | | : | : | : | : | : | : | : | : | : |
Db 235 PSFEELYKKTALWMYLTDFTEFPHPPFPNVLYIGGVLAQPAKPVSEELDFIAQSGEHG 294

Qy 295 FVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLANVKIVDWLPQ 354
| : : | | | : | | | : | : : | | : : | | : | | | : | : | : | : |
Db 295 FIIVTFGSMVPSNPLTEFVKEMNDGFSKIPQKVIWRYRISEWPKVLQLAPNVKIMNWISQ 354

Qy 355 SDLLAHPsirLfvthggqnsimeaiqhgvpmvgiplfgdqpenmvrveakkfgvsiqlkk 414
: | | | | | | | | | | | | | | | | | | | : | : | : | : | : | :
Db 355 NDLLGHPKARLLVTHGGVNSIQEAIYHGVPMVAIPLFFDQFDNAVRIKAKHLGTFIPKDQ 414

Qy 415 LKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKP 474
| | | | | : : : : | : : : : | : | | | : : | : : | : : | : | | |
Db 415 LKAEKLANAIRDVIGGESYKNSAMHLSLIQRSQPFPKDQQIVRWVEHIVKVGTDHLIPY 474

Qy 475 VFQQPWHEQYLFDFVFLVLLGLTLGLTLWLCGKLLGMAVWWLRGARKVKE 522
: | | : : | | | : : : : | : | | | : | : | : : : :
Db 475 SYQQPLYQQYLLDVFLFVFCVIGACYLTVKLLKMFQKLCSFRKLKQ 522

RESULT 9

Q8NAW4

ID Q8NAW4 PRELIMINARY; PRT; 221 AA.
AC Q8NAW4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ34658.
OS Homo sapiens (Human).


```

      |||||:||||:||||:|: ||| |||| | :|||:| :: |:| |
Db      61 IRLFVTHGGQNSVMEAIRHGVPMVGLPVNGDQHGNMVRVAKNYGVSIRLNQVTADTLTL 120

Qy      423 KMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHE 482
      |||::||||| ||||| | |||| |||||:||||| |||||
Db      121 TMKQVIEDKRYKSAVAASVILHSQPLSPAQRLVGWIDHILQTGGATHLKPYAFQQPWHE 180

Qy      483 QYLFDVVFVLLGLTLGLTLWLCCGKLLGMAVWWLRGARKVKET 523
      ||| |||||:|||||: |||||:|
Db      181 QYLIDVFVFLGLTLGLTMLWLCGKLLGVVARWLRGARKVKKT 221

```

RESULT 10

Q8IYS9

```

ID      Q8IYS9          PRELIMINARY;      PRT;      252 AA.
AC      Q8IYS9;
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Testis;
RA      Strausberg R.;
RL      Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC035012; AAH35012.1; -.
DR      GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR      GO; GO:0008152; P:metabolism; IEA.
DR      InterPro; IPR002213; UDP_glucos_trans.

```

DR Pfam; PF00201; UDPGT; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29155 MW; 956CC9F9718B8982 CRC64;

Query Match 33.0%; Score 914.5; DB 2; Length 252;
Best Local Similarity 75.7%; Pred. No. 6.5e-64;
Matches 171; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

Qy 58 HKRGPFM-PDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEY 116
|: | |: | |:||||||| |:||||: || ||::| | | |: |:|
Db 3 HQSGKFLIPDIKEEEKSYQVIRWFSPEDHQKRIKKHFD SYIETALDGRKESEALVKLMEI 62

Qy 117 LALQCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFSGSLEFG 176
|||: |:||||||| |:|:| || |:| ||||| ||||| |:|:|:|
Db 63 FGTQCSYLLSRKDIMDSLKNENYDLVFVEAFDFCSFLIAEKLVKPFVAILPTTFGSLDFG 122

Qy 177 LPIPLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPV 236
|| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 LPSPLSYVPVFPSSLTLDHMDFWGRVKNFLMFFSF SRSQWDMQSTFDNTIKEHFPEGSRPV 182

Qy 237 LSHLLKLAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQD 282
|||||||:|||||||:|||||||:|||||||:|||||||:
Db 183 LSHLLKLAELWFVNSDFAFDFARPLLNTVYIGGLMEKPIKPVPQN 228

RESULT 11

Q8BRY7

ID Q8BRY7 PRELIMINARY; PRT; 302 AA.
AC Q8BRY7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male aorta and vein cDNA, RIKEN full-length
DE enriched library, clone:A530069C13 product:hypothetical UDP-
DE glucoronosyl and UDP-glucosyl transferase containing protein, full
DE insert sequence.
GN Name=AI313915;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AK041045; BAC30796.1; -.
 DR MGD; MGI:2145969; AI313915.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002213; UDP_glucos_trans.
 DR Pfam; PF00201; UDPGT; 1.
 KW Hypothetical protein; Transferase.
 SQ SEQUENCE 302 AA; 35256 MW; C78A84C1D58987DC CRC64;

Query Match 28.6%; Score 792; DB 2; Length 302;
 Best Local Similarity 57.9%; Pred. No. 3.9e-54;
 Matches 157; Conservative 37; Mismatches 75; Indels 2; Gaps 2;

Qy 1 MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKR 60
 || | ||: || |:| |||||: |||:: |||:| : |||| | ::
 Db 1 MAAHRRWLLMSFLFLEVILLEAAKILTISTLSASHYIVISRVSQVLHEGGHNVTKLLYES 60

Qy 61 GPFMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQ 120
 :||:|: ||||:| ||| ::| || || | || : :|
 Db 61 AN-IPDFRKEKPSYQVINWRPPEDQEKKFADLRHRLTEEITYGRSKHHTLLKIHQYFGDL 119

Qy 121 CSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFSGSLEFGLP-I 179
 || |:||||| |||||:|::: | | |||| ||: | | ::|||
 Db 120 CSQLLSRKDIMDFLKNENFDLVLLDSMDLCSLLIVEKLGKRFVSFLPFQFSYMDFGPLSA 179

Qy 180 PLSYVPVFRSLTLDHMDFWGRVKNFLMFFSFCCRQOHMQSTFDNTIKEHFTEGSRPVLSH 239
 |||| ||: | ||| ||||| ||||| | :|: : | :|:|:| |||:| |||
 Db 180 PLSYAPVYGSLTDQMDFWGRVKNFLMFLDFSMKQREILSQYDSTIQEHFVEGSQPVLSD 239

Qy 240 LLLKAELWFINSDFAFDFARPLLNTVYVGG 270
 |||||:| |||| | |||| | |||||
 Db 240 LLLKAELWFVNSDFALDFARPLFPNTVYVGG 270

RESULT 12

UDC1_RABIT

ID UDC1_RABIT STANDARD; PRT; 502 AA.
 AC P36514;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE UDP-glucuronosyltransferase 2C1 microsomal (EC 2.4.1.17) (UDPGT)
 DE (Fragment).
 GN Name=UGT2C1; Synonyms=UGT2A2;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RX MEDLINE=93315511; PubMed=8325897;
 RA Tukey R.H., Pendurthi U.R., Nguyen N.T., Green M.D., Tephly T.R.;
 RT "Cloning and characterization of rabbit liver UDP-
 RT glucuronosyltransferase cDNAs. Developmental and inducible expression
 RT of 4-hydroxybiphenyl UGT2B13.";
 RL J. Biol. Chem. 268:15260-15266(1993).
 CC -!- FUNCTION: UDPGT is of major importance in the conjugation and
 CC subsequent elimination of potentially toxic xenobiotics and
 CC endogenous compounds.
 CC -!- CATALYTIC ACTIVITY: UDP-glucuronate + acceptor = UDP + acceptor
 CC beta-D-glucuronoside.
 CC -!- SUBCELLULAR LOCATION: Microsomal.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; L01083; AAA18023.1; -.
DR InterPro; IPR002213; UDP_glucos_trans.
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Glycoprotein; Glycosyltransferase; Microsome; Multigene family;
KW Transferase; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM 466 481 Potential.
FT CARBOHYD 177 177 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 288 288 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 502 AA; 57449 MW; B6E65670BFAE1D35 CRC64;

Query Match 27.0%; Score 748.5; DB 1; Length 502;
Best Local Similarity 35.4%; Pred. No. 2.1e-50;
Matches 180; Conservative 82; Mismatches 178; Indels 69; Gaps 14;

Qy 34 SHYLLMDRVSQILQDHGHNV-----MLNHKRGPFMPDFKK-----EE----- 71
|::: : : : | | : | : : | : : : | |
Db 7 SHWINLKVILEELQLRGHEITVLPSPSLLLDHTKIPFNVEVLQLQVTKETLMEELNTVL 66

Qy 72 --KSYQV--ISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHFLNR 127
|::: : | | | : | | : | | : | :
Db 67 YMSSFELPTLSWWKVLGKMVEMGKQFS-----KNLRRV-----CDSAITN 106

Qy 128 KDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFPVAILSTSFSGSLE----FGLPIPLSY 183
|::: | | : : : : | : | | | | | : : : | | | | |
Db 107 KELLDRLKAAKFDICLADPLAFCGELVAELLNIPFVYSFRFSIGNIIERSCAGLPTPSSY 166

Qy 184 VPVFRSLLTDHMDFWGRVKNFLMFFSFCCRQQH-MQSTFDNTIKEHFTE--GSRPVLSHL 240
| | | | : | | : : : : | | : | : : : | : :
Db 167 VPGSTSGLTDNMSFVQRLKNWLLYLMNDMMFSHFMLSEWD----EYYSKVLGRRTTICEI 222

Qy 241 LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKVPQDLENFIAKFGDSGFVLVTL 300
: | | : | : : | | | | | | | | : : : | : : | : |
Db 223 MGKAEMWLIRSYWDFEFPRPFLPNFEYVGGLHCKPAKPLPEELEEFVQSSGNDGVVVFTL 282

Qy 301 GSMVNTCQNPEIFKEMNN----AFAHLPQGVIWKQCQSHWPKDVHLAANVKIVDWLPQSD 356
| | : | : : | | : | : | : | : | : : : | : : | : : |
Db 283 GSMI---QN--LTEERSNLIASALAQIPQKVLWRYT---GKKPATLGPNTRLFEWIPQND 334

Qy 357 LLAHPSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLK 416
| | | | : | | : | | | | | | | | | : : | : : : :
Db 335 LLGHPKTRAFITHGGTNGLYEAIYHGVPVVGIPFLFGDQPDNIARVKAKGAADVVDLRIMT 394

Qy 417 AETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVF 476
: | : : : | : | | | | | : : : | : : | : | :
Db 395 TSSLLKALKDVINNPYSKENAMKLSRIHHDQPLKPLDRAVFWIEFVMRHKGARHLRVAAH 454

Qy 477 QQPWHEQYLFDFVFLGLTLGLTLWLCGK 505
| : | | | | : : | |
Db 455 DLTWFQYYSLDVVVFLLTVCVATIIIFLAKK 483

098TB5

Query Match 26.3%; Score 727; DB 2; Length 541;
Best Local Similarity 33.3%; Pred. No. 1.2e-48;
Matches 166; Conservative 99; Mismatches 199; Indels 34; Gaps 10;

Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDGHGNVTMLNHRKGPMPDFKKEE	71
Db	11	LWSAVGIARAAKIVVPPIMFESHLYIFKTLASALHDQGHQTVFLLSEGREIPPSNHYRL	70
Qy	72	KSYQVISWLAPEDHQREFKKS-FDFFLEETL---GGRGKFENLLNVLEYLALQCSHFLN	126
Db	71	KRYPGI-----FNSSTSDDFLQSKMRSIFSGRLTALELFDILDHYSKNCDMIVG	119
Qy	127	RKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGKPFVAILSTSFGSLEFGLPIPLSYVPV	186
Db	120	NQNLMHALKQEKFDLLLVDPNEMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPAPLSYVPE	179
Qy	187	FRSLLTDHMDFWGRVKNFLMF-----FSFCRRQOHMQSTFDNTIKEHFTEGSRPVLSHL	240
Db	180	FNSLLTDRMNLFERMKNTFVYVISRFGVSFL-----VLPKYERIMQKHKVLPERSMYD-L	233
Qy	241	LLKAELWFINSDFAFDFARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTL	300

Db 234 VHGSSIWMLCTDIALEFPRPTLPNVVYVGILTKPASPLPEDLQTWVNGANENGFLVVSF 293
 Qy 301 GSMVNTCQNPEIFKEMNNAFAHLPQGVWKCQCCHWPKDVHLAANVKIVDWLPQSDLLAH 360
 | : | : : : | | | | : : | : | | : : | | | |
 Db 294 GAGVKYL-SEDVANKLARALARLPQRVIWRFSGN---KPRNLGNNTKLEIWLQNDLLGH 349
 Qy 361 PSIRLFVTHGGQNSIMEAIQHGVPMVGIPFLGDQPENMVRVEAKKFGVSIQLKKLKAETL 420
 | : | : : | | | : | | : | | | | : | | : | : | :
 Db 350 PNIKAFLSHGGLNSIFETMYHGVVVGIPFLGDHYDTMTRVQAKGMGILLNWKTVTESEL 409
 Qy 421 ALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYPVQQPW 480
 : : : : | : | : | : | : | : : : | | : :
 Db 410 YEALEKVINDPSYRQRAQLSEIHKDQPGHPVNRTVYWINYILRHNGAQHLRAAVYSISL 469
 Qy 481 HEQYLFDV-FVFLGLTL 497
 : : : | : | : |
 Db 470 YQYFLLDIAFVVLVGAAL 487

RESULT 14

Q6UWM9

ID Q6UWM9 PRELIMINARY; PRT; 527 AA.
 AC Q6UWM9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RSDK2559 (UDP-glucuronosyltransferase).
 GN Name=UGT2A3; ORFNames=UNQ2559;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Court M.H.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 DR EMBL; AY358727; AAQ89089.1; -.
 DR EMBL; AY542891; AAS48425.1; -.
 DR GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.

DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR006121; HeavyMe_transpt.
 DR InterPro; IPR002213; UDP_glucos_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS01047; HMA_1; UNKNOWN_1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Glycosyltransferase; Transferase.
 SQ SEQUENCE 527 AA; 60284 MW; EB6C8F886B4DEC5E CRC64;

Query Match 25.8%; Score 714.5; DB 2; Length 527;
 Best Local Similarity 33.9%; Pred. No. 1.1e-47;
 Matches 172; Conservative 93; Mismatches 208; Indels 35; Gaps 13;

Qy	34	SHYLLMDRVSQILQDHGHNVTMLNHKRGPFMPDFKKEEK-SYQVISWLPAPEDHQREFKKS	92
		: : : : : : : : :	
Db	34	SHWLNKLVILEELIVRGHEVTVLTHSK-PSLIDYRKPSALKFEVVH--MPQDRTEENEIF	90
Qy	93	FDFLEETLGGRGKFENLLNVLEY-----LALQCSHFLNRKDIMDSLKNENFDMVIVE	145
		: : : : : : : : : : : : :	
Db	91	VDLAL-NVLPGLSTWQSVIKLNDFFVEIRGTLKMMCESFIYNQTLMKKLQETNYDVMLID	149
Qy	146	TFDYCPFLIAEKLGPFAVAILSTSF-GSLEFG---LPIPLSYVPVFRSLLTDHMDFWGRV	201
		: : : :	
Db	150	PVIPCGDLMAELLAVPFVLTLRISVGGNMERSCGKLPAPLSYVPVPMPTGLTDRMTFLERV	209
Qy	202	KNFLMFFSFCRRQQHMQSTFDNTIKEHFTE---GSRPVLSHLLLKAEWFINSDFAFDFA	258
		: : : : : : : :	
Db	210	KNSMLSVLF----HFWIQDYDYHFWEEFYSKALGRPTTLCETVGKAEIWLIRTYWDFEFP	265
Qy	259	RPLLNTVYVGGLEMEKPIKVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNN	318
		: : : : : : : : : :	
Db	266	QPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGEDGIVVFSLSLGF---QN--VTEEKAN	320
Qy	319	----AFAHLPQGVWKCQCSHWPKDVHLANVKIVDWLPQSDLLAHPSIRLFVTHGGQNS	374
		: : : : : : : : : :	
Db	321	IIASALAQIPQKVLWRYK---GKKPSTLGANTRYDWIPQNDLLGHPKTKAFITHGGMNG	377
Qy	375	IMEAIQHGVPMVGPIPLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK	434
		: : : : : : : : : :	
Db	378	IYEAIIYHGVPMVGVPPIFGDQLDNIAHMKAKGAAVEINFKTMTSEDLLRALRTVITDSSYK	437
Qy	435	SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYVFQQPWHEQYLFDFVVFLLG	494
		: : : : : :	
Db	438	ENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSAHDLTWQHYSIDVIGFLLT	497
Qy	495	LTLGTLWLWLCGKLLGMAVWWLRGARKVKE	522
		: : : : : :	
Db	498	CVATAIFLFTKCFLFSCQKFNKTRKIEK	525

RESULT 15

CGT_HUMAN

ID CGT_HUMAN STANDARD; PRT; 541 AA.
 AC Q16880; O00196;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE 2-hydroxyacylsphingosine 1-beta-galactosyltransferase precursor
 DE (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Ceramide
 DE UDP-galactosyltransferase) (Cerebroside synthase).
 GN Name=UGT8; Synonyms=CGT, UGT4;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96299661; PubMed=8661025; DOI=10.1006/geno.1996.0242;
 RA Bosio A., Binczek E., Lebeau M.M., Fernald A.A., Stoffel W.;
 RT "The human gene CGT encoding the UDP-galactose ceramide galactosyl
 RT transferase (cerebroside synthase): cloning, characterization, and
 RT assignment to human chromosome 4, band q26.";
 RL Genomics 34:69-75(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97242209; PubMed=9125199; DOI=10.1006/bbrc.1997.6240;
 RA Kapitonov D.E., Yu R.K.;
 RT "Cloning, characterization, and expression of human ceramide
 RT galactosyltransferase cDNA.";
 RL Biochem. Biophys. Res. Commun. 232:449-453(1997).
 CC -!- FUNCTION: Catalyzes the transfer of galactose to ceramide, a key
 CC enzymatic step in the biosynthesis of galactocerebrosides, which
 CC are abundant sphingolipids of the myelin membrane of the central
 CC nervous system and peripheral nervous system.
 CC -!- CATALYTIC ACTIVITY: UDP-galactose + 2-(2-hydroxyacyl)sphingosine =
 CC UDP + 1-(beta-D-galactosyl)-2-(2-hydroxyacyl)sphingosine.
 CC -!- PATHWAY: Galactocerebroside biosynthesis.
 CC -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR EMBL; U30930; AAC50565.1; -.
 DR EMBL; U32370; AAC50815.1; -.
 DR EMBL; U31353; AAC50815.1; JOINED.
 DR EMBL; U31461; AAC50815.1; JOINED.
 DR EMBL; U31658; AAC50815.1; JOINED.
 DR EMBL; U31861; AAC50815.1; JOINED.
 DR EMBL; U62899; AAC51187.1; -.
 DR Genew; HGNC:12555; UGT8.
 DR MIM; 601291; -.
 DR GO; GO:0008489; F:UDP-galactose-glucosylceramide beta-1,4-gal. . .; TAS.
 DR GO; GO:0007417; P:central nervous system development; TAS.
 DR GO; GO:0007422; P:peripheral nervous system development; TAS.
 DR InterPro; IPR002213; UDP_glucos_trans.
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW Glycoprotein; Glycosyltransferase; Microsome; Signal; Transferase;
 KW Transmembrane.

FT	SIGNAL	1	20	Potential.
FT	CHAIN	21	541	2-hydroxyacylsphingosine 1-beta-
FT				galactosyltransferase.
FT	TRANSMEM	472	492	Potential.
FT	CARBOHYD	78	78	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	333	333	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	442	442	N-linked (GlcNAc. . .) (Potential).
FT	CONFLICT	99	99	T -> P (in Ref. 2).
FT	CONFLICT	116	116	L -> M (in Ref. 2).
FT	CONFLICT	356	356	L -> V (in Ref. 2).
FT	CONFLICT	379	379	L -> V (in Ref. 2).
SQ	SEQUENCE	541 AA;	61455 MW;	EC532798F7E15834 CRC64;

Query Match 25.3%; Score 699; DB 1; Length 541;
 Best Local Similarity 32.2%; Pred. No. 1.9e-46;
 Matches 166; Conservative 95; Mismatches 185; Indels 70; Gaps 12;

Qy	13	LLPGVLLSEAAKILTISTV-GGSHYLLMDRVSQILQDHGHN-VTMLNHKRGPFMPDFKKE	70
		:: : : : : :: : : ::	
Db	11	LWSAVGIAKAAKIIIVPPIMFESHMYIFKTLASALHERGHHTVFLLEGRD-----	61
Qy	71	EKSQVISWLPEDHQ--REFKKSF-----DFFLEETL----GGRGKFENLLNVLEYLAL	119
		: : : : : : :::	
Db	62	-----IAPSNHYSLQRYPGIFNSTTSDAFLQSKMRNIFSGRLTAIELFDILDHYTK	112
Qy	120	QCSHFLNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSFGSLEFGLPI	179
		: :: :: : : : :	
Db	113	NCDLMVGNHALIQGLKKEKFDLLLVDPNDMCGFVIAHLLGVKYAVFSTGLWYPAEVGAPA	172
Qy	180	PLSYVPVFRSLLTDHMDFWGRVKN-----FLMFFSFCCRQQHM-----QSTFD	222
		: : : : : :	
Db	173	PLAYVPEFNSLLTDRMNLQRMKNTGVYLISRLGVSVFLVLPKYERIMQYNLLPEKSMYD	232
Qy	223	NTIKEHFTEGSRPVLSHLLKAEWFINSDFAFDFARPLLNTVYVGGLMKPIKPVPQD	282
		: : : : : : : :	
Db	233	-----LVHGSSLWMLCTDVALEFPRTLPNVVYVGGILTKPASPLPED	275
Qy	283	LENFIAKFGDSGFVLVTLGSMVNTCQNPEIFKEMNNAFAHLPQGVIWKCQCSHWPKDVHL	342
		: :: : : : : : : : :	
Db	276	LQRWVNGANEHGFVLVSFGAGVKYL-SEDIANKLAGALGRLPQKVIWRFS---GPKPKNL	331
Qy	343	AANVKIVDWLPQSDLLAHPsirLfvTHGGQNSIMEAIQHGVPMVGIPLFGDQPENMVRVE	402
		:: : : : : : : :	
Db	332	GNNTKLIEWLPQNDLLGHSKIAFLSHGGLNSIFETMYHGVVVGIPLFGDHYDTMTRVQ	391
Qy	403	AKKFGVSIQLKKLKAETLALKMKQIMEDKRYKSAAVAASVILRSHPLSPTQRLVGWIDHV	462
		: : : : : : : : : : : :	
Db	392	AKGMGILLEWKTVTEKELYEALVKVINNPYSYRQRAQKLSEIHKDQPGHPVNRTIYWIDYI	451
Qy	463	LQTGGATHLKPYVFQQPWHEQYLFDV-FVLLGLTL	497
		:: : : : : :	
Db	452	IRHNGAHLRAAVHQISFCQYFLLDIAFVLLLGAAL	487

Search completed: February 15, 2005, 12:57:51
 Job time : 150 secs